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- (54) **PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING STAPHYLOCOCCUS AUREUS**
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(57) **ABSTRACT**

Disclosed are novel immunogenic proteins derived from *Staphylococcus aureus*, as well as methods for their use in conferring protective immunity against *S. aureus* infections. Also disclosed are nucleic acids encoding the proteins and methods of use of these nucleic acids.

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**PROTEINS AND NUCLEIC ACIDS USEFUL
IN VACCINES TARGETING
STAPHYLOCOCCUS AUREUS**

CROSS-REFERENCE TO RELATED
APPLICATIONS

In accordance with 37 C.F.R. 1.76, a claim of priority is included in an Application Data Sheet filed concurrently herewith. Accordingly, the present invention claims priority as a continuation of U.S. patent application Ser. No. 14/802,602, entitled "PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING *STAPHYLOCOCCUS AUREUS*", filed Jul. 17, 2015, now U.S. Pat. No. 9,534,022, issued Jan. 3, 2017, which claims priority as a divisional of U.S. patent application Ser. No. 14/110,475, entitled "PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING *STAPHYLOCOCCUS AUREUS*", filed Nov. 25, 2013, now U.S. Pat. No. 9,085,631, issued Jul. 21, 2015, which is a § 371 national stage entry of International Application No. PCT/EP2012/056069, entitled "PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING *STAPHYLOCOCCUS AUREUS*", filed Apr. 3, 2012, which claims priority to Danish Patent Application No. PA 2011 70167, entitled "PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING *STAPHYLOCOCCUS AUREUS*", filed Apr. 8, 2011 and U.S. Provisional Application No. 61/473,376, entitled "PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING *STAPHYLOCOCCUS AUREUS*", filed Apr. 8, 2011, the entire contents of which are incorporated herein by reference.

FIELD OF THE INVENTION

The present invention relates to the field of antimicrobial prophylaxis and therapy. In particular the present invention relates to novel proteins and polynucleotides derived from *Staphylococcus aureus*. The invention further relates to vectors comprising the polynucleotides, transformed host organisms expressing the polynucleotides, antibodies (mono- or polyclonal) specific for the polypeptides as well as diagnostic, prophylactic and therapeutic uses and methods. Finally, also methods of preparation are part of the invention.

BACKGROUND OF THE INVENTION

Bacterial infections are in most instances successfully treated by administration of antibiotics to patients in need thereof. However, due to careless or thoughtless use of powerful antibiotics, many pathological germs become resistant against antibiotics over time. One threatening example is *Staphylococcus aureus*. In particular in hospitals this bacterium is of relevance. So-called Methicillin Resistant *S. aureus* (MRSA) strains jeopardize patient's survival in hospitals, in particular after surgery.

Vaccination is considered to be a very effective method of preventing infectious diseases in human and veterinary health care. Vaccination is the administration of immunogenically effective amounts of antigenic material (the vaccine) to produce immunity to a disease/disease-causing pathogenic agent. Vaccines have contributed to the eradication of smallpox, the near eradication of polio, and the control of a variety of diseases, including rubella, measles, mumps, chickenpox, typhoid fever.

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Before "the genomic era", vaccines were based on killed or live attenuated, microorganisms, or parts purified from them. Subunit vaccines are considered as a modern upgrade of these types of vaccine, as the subunit vaccines contain one or more protective antigens, which are more or less the weak spot of the pathogen. Hence, in order to develop subunit vaccines, it is critical to identify the proteins, which are important for inducing protection and to eliminate others.

An antigen is said to be protective if it is able to induce protection from subsequent challenge by a disease-causing infectious agent in an appropriate animal model following immunization.

The empirical approach to subunit vaccine development, which includes several steps, begins with pathogen cultivation, followed by purification into components, and then testing of antigens for protection. Apart from being time and labour consuming, this approach has several limitations that can lead to failure. It is not possible to develop vaccines using this approach for microorganisms, which cannot easily be cultured and only allows for the identification of the antigens, which can be obtained in sufficient quantities. The empirical approach has a tendency to focus on the most abundant proteins, which in some cases are not immunoprotective. In other cases, the antigen expressed during in vivo infection is not expressed during in vitro cultivation. Furthermore, antigen discovery by use of the empirical approach demands an extreme amount of proteins in order to discover the protective antigens, which are like finding needles in the haystack. This renders it a very expensive approach, and it limits the vaccine development around diseases, which is caused by pathogens with a large genome or disease areas, which perform badly in a cost-effective perspective.

OBJECT OF THE INVENTION

It is an object of embodiments of the invention to provide *S. aureus* derived antigenic polypeptides that may serve as constituents in vaccines against *S. aureus* infections and in diagnosis of *S. aureus* infections. It is also an object to provide nucleic acids, vectors, transformed cells, vaccine compositions, and other useful means for molecular cloning as well as for therapy and diagnosis with relevance for *S. aureus*.

SUMMARY OF THE INVENTION

It has been found by the present inventor(s) that *S. aureus*, in particular drug resistant *S. aureus*, expresses a number of hitherto unknown surface exposed proteins which are candidates as vaccine targets as well as candidates as immunizing agents for preparation of antibodies that target *S. aureus*.

So, in a first aspect the present invention relates to a polypeptide comprising

a) an amino acid sequence selected from the group consisting of any one of SEQ ID NOs: 1-19, or

b) an amino acid sequence consisting of at least 5 contiguous amino acid residues from any one of SEQ ID NOs: 1-19, or

c) an amino acid sequence having a sequence identity of at least 60% with the amino acid sequence of a),

d) an amino acid sequence having a sequence identity of at least 60% with the amino acid sequence of b), or

e) an assembly of amino acids derived from any one of SEQ ID NOs: 1-19 which has essentially the same 3D

conformation as in the protein from which said assembly is derived so as to constitute a B-cell epitope,

said polypeptide being antigenic in a mammal.

In another aspect, the invention relates to an isolated nucleic acid fragment, which comprises

i) a nucleotide sequence encoding a polypeptide of the invention, or

ii) a nucleotide sequence consisting of any one of SEQ ID NOs: 20-57.

iii) a nucleotide sequence consisting of at least 10 consecutive nucleotides in any one of SEQ ID NOs: 20-57,

iv) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in i) or ii),

v) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in iii),

vi) a nucleotide sequence complementary to the nucleotide sequence in i)-v), or

vii) a nucleotide sequence which hybridizes under stringent conditions with the nucleotide sequence in i)-vi).

In a third aspect, the invention relates to a vector comprising the nucleic acid of the invention, such as a cloning vector or an expression vector.

In fourth aspect, the invention relates to a cell which is transformed so as to carry the vector of the invention.

In a fifth aspect, the invention relates to a pharmaceutical composition comprising a polypeptide of the invention, a nucleic acid fragment of the invention, a vector of the invention, or a transformed cell of the invention, and a pharmaceutically acceptable carrier, vehicle or diluent.

In a sixth aspect, the invention relates to a method for inducing immunity in an animal by administering at least once an immunogenically effective amount of a polypeptide of the invention, a nucleic acid fragment of the invention, a vector of the invention, a transformed cell of the invention, or a pharmaceutical composition of the fifth aspect of the invention so as to induce adaptive immunity against *S. aureus* in the animal.

In a seventh and eighth aspect, the invention relates to 1) a polyclonal antibody in which the antibodies specifically bind to at least one polypeptide of the invention, and which is essentially free from antibodies binding specifically to other *S. aureus* polypeptides, and to 2) an isolated monoclonal antibody or antibody analogue which binds specifically to a polypeptide of the invention. In a related ninth aspect, the invention relates to a pharmaceutical composition comprising such a polyclonal or monoclonal antibody and a pharmaceutically acceptable carrier, vehicle or diluent.

In a 10th aspect, the invention relates to a method for prophylaxis, treatment or amelioration of infection with *S. aureus*, in particular infection with multi-resistant *S. aureus*, comprising administering a therapeutically effective amount of an antibody of the 7th or 8th aspect of the invention or a pharmaceutical composition of the eighth aspect to an individual in need thereof.

In an 11th aspect, the invention relates to a method for determining, quantitatively or qualitatively, the presence of *S. aureus*, in particular the presence of multi-resistant *S. aureus*, in a sample, the method comprising contacting the sample with an antibody of aspects 8 or 9 of the invention and detecting the presence of antibody bound to material in the sample.

In an 12th aspect of the invention is provided a method for determining, quantitatively or qualitatively, the presence of antibodies specific for *S. aureus*, in particular the presence of antibodies specific for multi-resistant *S. aureus*, in a sample, the method comprising contacting the sample with

a polypeptide of the invention and detecting the presence of antibody that specifically bind said polypeptide.

In a 13th aspect, the invention relates to a method for determining, quantitatively or qualitatively, the presence of a nucleic acid characteristic of *S. aureus*, in particular the presence of a nucleic acid characteristic of multi-resistant *S. aureus*, in a sample, the method comprising contacting the sample with a nucleic acid fragment of the invention and detecting the presence of nucleic acid in the sample that hybridizes to said nucleic acid fragment.

In a 14th aspect, the invention relates to a method for the preparation of the polypeptide of the invention, comprising culturing a transformed cell of the present invention, which is capable of expressing the nucleic acid of the invention, under conditions that facilitate that the transformed cell expresses the nucleic acid fragment of the invention, which encodes a polypeptide of the invention, and subsequently recovering said polypeptide, or preparing said polypeptide by means of solid or liquid phase peptide synthesis.

In a 15th aspect, the invention relates to a method for determining whether a substance, such as an antibody, is potentially useful for treating infection with *S. aureus*, the method comprising contacting the polypeptide of the invention with the substance and subsequently establishing whether the substance has at least one of the following characteristics:

- 1) the ability to bind specifically to said polypeptide,
- 2) the ability to compete with said polypeptide for specific binding to a ligand/receptor, and
- 3) the ability to specifically inactivate said polypeptide.

Finally, in a 16th aspect, the invention relates to a method for determining whether a substance, such as a nucleic acid, is potentially useful for treating infection with *S. aureus*, the method comprising contacting the substance with the nucleic acid fragment of claim of the invention and subsequently establishing whether the substance has either the ability to

- 1) bind specifically to the nucleic acid fragment, or
- 2) bind specifically to a nucleic acid that hybridizes specifically with the nucleic acid fragment.

DETAILED DISCLOSURE OF THE INVENTION

Definitions

The term "polypeptide" is in the present context intended to mean both short peptides of from 2 to 10 amino acid residues, oligopeptides of from 11 to 100 amino acid residues, and polypeptides of more than 100 amino acid residues. Further-more, the term is also intended to include proteins, i.e. functional biomolecules comprising at least one polypeptide; when comprising at least two polypeptides, these may form complexes, be covalently linked, or may be non-covalently linked. The polypeptide (s) in a protein can be glycosylated and/or lipidated and/or comprise prosthetic groups.

The term "subsequence" means any consecutive stretch of at least 3 amino acids or, when relevant, of at least 3 nucleotides, derived directly from a naturally occurring amino acid sequence or nucleic acid sequence, respectively

The term "amino acid sequence" is the order in which amino acid residues, connected by peptide bonds, lie in the chain in peptides and proteins.

The term "adjuvant" has its usual meaning in the art of vaccine technology, i.e. a substance or a composition of matter which is 1) not in itself capable of mounting a specific

immune response against the immunogen of the vaccine, but which is 2) nevertheless capable of enhancing the immune response against the immunogen. Or, in other words, vaccination with the adjuvant alone does not provide an immune response against the immunogen, vaccination with the immunogen may or may not give rise to an immune response against the immunogen, but the combined vaccination with immunogen and adjuvant induces an immune response against the immunogen which is stronger than that induced by the immunogen alone.

“Sequence identity” is in the context of the present invention determined by comparing 2 optimally aligned sequences of equal length (e.g. DNA, RNA or amino acid) according to the following formula: $(N_{ref}-N_{dif}) \cdot 100 / N_{ref}$, wherein N_{ref} is the number of residues in one of the 2 sequences and N_{dif} is the number of residues which are non-identical in the two sequences when they are aligned over their entire lengths and in the same direction. So, two sequences 5'-ATTCGGAACC-3' (SEQ ID NO: 58) and 5'-ATACGGGACC-3' (SEQ ID NO: 58) will provide the sequence identity 80% ($N_{ref}=10$ and $N_{dif}=2$).

An “assembly of amino acids” means two or more amino acids bound together by physical or chemical means.

The “3D conformation” is the 3 dimensional structure of a biomolecule such as a protein. In monomeric polypeptides/ proteins, the 3D conformation is also termed “the tertiary structure” and denotes the relative locations in 3 dimensional space of the amino acid residues forming the polypeptide.

“An immunogenic carrier” is a molecule or moiety to which an immunogen or a hapten can be coupled in order to enhance or enable the elicitation of an immune response against the immunogen/hapten. Immunogenic carriers are in classical cases relatively large molecules (such as tetanus toxoid, KLH, diphtheria toxoid etc.) which can be fused or conjugated to an immunogen/hapten, which is not sufficiently immunogenic in its own right—typically, the immunogenic carrier is capable of eliciting a strong T-helper lymphocyte response against the combined substance constituted by the immunogen and the immunogenic carrier, and this in turn provides for improved responses against the immunogen by B-lymphocytes and cytotoxic lymphocytes. More recently, the large carrier molecules have to a certain extent been substituted by so-called promiscuous T-helper epitopes, i.e. shorter peptides that are recognized by a large fraction of HLA haplotypes in a population, and which elicit T-helper lymphocyte responses.

A “T-helper lymphocyte response” is an immune response elicited on the basis of a peptide, which is able to bind to an MHC class II molecule (e.g. an HLA class II molecule) in an antigen-presenting cell and which stimulates T-helper lymphocytes in an animal species as a consequence of T-cell receptor recognition of the complex between the peptide and the MHC Class II molecule present.

An “immunogen” is a substance of matter which is capable of inducing an adaptive immune response in a host, whose immune system is confronted with the immunogen. As such, immunogens are a subset of the larger genus “antigens”, which are substances that can be recognized specifically by the immune system (e.g. when bound by antibodies or, alternatively, when fragments of the are antigens bound to MHC molecules are being recognized by T-cell receptors) but which are not necessarily capable of inducing immunity—an antigen is, however, always capable of eliciting immunity, meaning that a host that has an established memory immunity against the antigen will mount a specific immune response against the antigen.

A “hapten” is a small molecule, which can neither induce nor elicit an immune response, but if conjugated to an immunogenic carrier, antibodies or TCRs that recognize the hapten can be induced upon confrontation of the immune system with the hapten carrier conjugate.

An “adaptive immune response” is an immune response in response to confrontation with an antigen or immunogen, where the immune response is specific for antigenic determinants of the antigen/immunogen—examples of adaptive immune responses are induction of antigen specific antibody production or antigen specific induction/activation of T helper lymphocytes or cytotoxic lymphocytes.

A “protective, adaptive immune response” is an antigen-specific immune response induced in a subject as a reaction to immunization (artificial or natural) with an antigen, where the immune response is capable of protecting the subject against subsequent challenges with the antigen or a pathology-related agent that includes the antigen. Typically, prophylactic vaccination aims at establishing a protective adaptive immune response against one or several pathogens.

“Stimulation of the immune system” means that a substance or composition of matter exhibits a general, non-specific immunostimulatory effect. A number of adjuvants and putative adjuvants (such as certain cytokines) share the ability to stimulate the immune system. The result of using an immunostimulating agent is an increased “alertness” of the immune system meaning that simultaneous or subsequent immunization with an immunogen induces a significantly more effective immune response compared to isolated use of the immunogen.

Hybridization under “stringent conditions” is herein defined as hybridization performed under conditions by which a probe will hybridize to its target sequence, to a detectably greater degree than to other sequences. Stringent conditions are target-sequence-dependent and will differ depending on the structure of the polynucleotide. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which are 100% complementary to a probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. Generally, stringent wash temperature conditions are selected to be about 5° C. to about 2° C. lower than the melting point (T_m) for the specific sequence at a defined ionic strength and pH. The melting point, or denaturation, of DNA occurs over a narrow temperature range and represents the disruption of the double helix into its complementary single strands. The process is described by the temperature of the midpoint of transition, T_m , which is also called the melting temperature. Formulas are available in the art for the determination of melting temperatures.

The term “animal” is in the present context in general intended to denote an animal species (preferably mammalian), such as *Homo sapiens*, *Canis domesticus*, etc. and not just one single animal. However, the term also denotes a population of such an animal species, since it is important that the individuals immunized according to the method of the invention substantially all will mount an immune response against the immunogen of the present invention.

As used herein, the term “antibody” refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An “antibody combining site” is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features

of an epitope of an antigen, which allows a binding of the antibody with the antigen. “Antibody” includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanised antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

“Specific binding” denotes binding between two substances which goes beyond binding of either substance to randomly chosen substances and also goes beyond simple association between substances that tend to aggregate because they share the same overall hydrophobicity or hydrophilicity. As such, specific binding usually involves a combination of electrostatic and other interactions between two conformationally complementary areas on the two substances, meaning that the substances can “recognize” each other in a complex mixture.

The term “vector” is used to refer to a carrier nucleic acid molecule into which a heterologous nucleic acid sequence can be inserted for introduction into a cell where it can be replicated and expressed. The term further denotes certain biological vehicles useful for the same purpose, e.g. viral vectors and phage—both these infectious agents are capable of introducing a heterologous nucleic acid sequence

The term “expression vector” refers to a vector containing a nucleic acid sequence coding for at least part of a gene product capable of being transcribed. In some cases, when the transcription product is an mRNA molecule, this is in turn translated into a protein, polypeptide, or peptide.

Specific Embodiments of the Invention

The Polypeptides of the Invention

In some embodiments the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention constitute at least 6, such as at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27 at least 28, at least 29, at least 30, at least 31, at least 32, at least 33, at least 34, and at least 35 contiguous amino acid residues. The number can be higher, for all of SEQ ID NOs. 1-19 at least 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, and at least 124 contiguous amino acid residues. Another way to phrase this is that for each of SEQ ID NOs: 1-19, the number of the contiguous amino acid residues is at least N-n, where N is the length of the sequence ID in question and n is any integer between 6 and N-1; that is, the at least 5 contiguous amino acids can be at least any number between 5 and the length of the reference sequence minus one, in increments of one.

In some embodiments, the polypeptide of the invention also has a sequence identity with the amino acid sequence of a) defined above of at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%. Similarly, the polypeptide of the invention in some embodiments also has a sequence identity with the amino acid sequence of b) defined above of at least 60%, such as at least 65%, at least 70%, at least 75%, at least 80%, at least 85%,

at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, and 128 in any one of SEQ ID NOs: 1-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, and 140 in any one of SEQ ID NOs: 1, 2, and 4-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 141, 142, 143, 144, 145, 146, 147, 148, 149, and 150 in any one of SEQ ID NOs: 1, 2, and 4-6, and 8-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, and 180 in any one of SEQ ID NOs: 2, 4-6, and 8-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 181, 182, 183, 184,

185, and 186 in any one of SEQ ID NOs: 4-6, and 8-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, and 204 in any one of SEQ ID NOs: 4-6, 8-11, 13-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to amino acid residue 205 in any one of SEQ ID NOs: 4-6, 8-11, 13-15, and 17-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, and 223 in any one of SEQ ID NOs: 4-6, 8-10, 13-15, and 17-19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 224, 225, 226, and 227 in any one of SEQ ID NOs: 4-6, 8-10, 13-15, 18, and 19, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303,

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In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 393, 394, 395, 396, 397, 398, 399, and 400 in any one of SEQ ID NOs: 4-6, 8-10, 13, 15, and 18, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, and 482 in any one of SEQ ID NOs: 4-6, 8-10, 13, and 15, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, and 605 in any one of SEQ ID NOs: 4-6, 8, 10, 13, and 15, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, and 765 in any one of SEQ ID NOs: 4, 5, 8, 10, 13, and 15, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, and 989 in any one of SEQ ID NOs: 4, 5, 8, 10, and 13, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, and 1005, in any one of SEQ ID NOs: 5, 8, 10, and 13, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than

$N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, and 1253 in any one of SEQ ID NOs: 5, 8, and 10, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, and 1270 in SEQ ID NO: 5 or 10, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than $N-L+1$, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b).

In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345,

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 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029,
 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038,
 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047,
 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056,
 2057, 2058, 2059, 2060, 2061, and 2062 in SEQ ID NO: 5,
 if the length of the at least 5 amino acid residues so
 permit—if the length of the at least 5 amino acids are higher
 than 5, the N-terminal first residue will not be higher
 numbered than N-L+1, where N is the number of amino acid
 residues of the reference sequence and L is the number of
 amino acids defined for option b.
 The polypeptide of the invention is in certain embod-
 iments also fused or conjugated to an immunogenic carrier
 molecule; or, phrased otherwise, the polypeptide of the
 invention also includes such an immunogenic carrier mol-
 ecule in addition to the material derived from SEQ ID NOs.
 1-19. The immunogenic carrier molecule is a typically
 polypeptide that induces T-helper lymphocyte responses in a
 majority of humans, such as immunogenic carrier proteins
 selected from the group consisting of keyhole limpet hemo-
 cyanino or a fragment thereof, tetanus toxoid or a fragment
 thereof, diphtheria toxoid or a fragment thereof. Other
 suitable carrier molecules are discussed infra.
 In preferred embodiments, the polypeptide of the inven-
 tion detailed above is capable of inducing an adaptive
 immune response against the polypeptide in a mammal, in
 particular in a human being. Preferably, the adaptive
 immune response is a protective adaptive immune response
 against infection with *S. aureus*, in particular multi-resistant
S. aureus. The polypeptide may in these cases induce a
 humeral and/or a cellular immune response.
 Epitopes
 SEQ ID NOs: 1-19 include antigenic determinants
 (epitopes) that are as such recognized by antibodies and/or
 when bound to MHC molecules by T-cell receptors. For the
 purposes of the present invention, B-cell epitopes (i.e.
 antibody binding epitopes) are of particular relevance.
 It is relatively uncomplicated to identify linear B-cell
 epitopes—one very simple approach entails that antibodies
 raised against *S. aureus* or *S. aureus* derived proteins dis-
 closed herein are tested for binding to overlapping oligo-
 meric peptides derived from any one of SEQ ID NO: 1-19.
 Thereby, the regions of the *S. aureus* polypeptide which are
 responsible for or contribute to binding to the antibodies can
 be identified.
 Alternatively, or additionally, one can produce mutated
 versions of the polypeptides of the invention, e.g. version
 where each single non-alanine residue in SEQ ID NOs.: 1-19
 are point mutated to alanine—this method also assists in
 identifying complex assembled B-cell epitopes; this is the
 case when binding of the same antibody is modified by
 exchanging amino acids in different areas of the full-length
 polypeptide.
 Also, in silico methods for B-cell epitope prediction can
 be employed: useful state-of-the-art systems for β -turn pre-
 diction is provided in Petersen B et al. (November 2010),
 Plos One 5(11): e15079; prediction of linear B-cell epitopes,
 cf: Larsen J E P et al. (April 2006), Immunome Research,

2:2; prediction of solvent exposed amino acids: Petersen B et al (July 2009), BMC Structural Biology, 9:51.

The Nucleic Acid Fragments of the Invention

The nucleic acid fragment of the invention referred to above is preferably is a DNA fragment (such as SEQ ID NOs: 20-38) or an RNA fragment (such as SEQ ID NOs 29-58).

The nucleic acid fragment of the invention typically consists of at least 11, such as at least 12, at least 13, at least 14, at least 15, at least 16, at least 17 at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, at least 30, at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, at least 41, at least 42, at least 43, at least 44, at least 45, at least 46, at least 47, at least 48, at least 49, at least 50, at least 51, at least 52, at least 53, at least 54, at least 55, at least 56, at least 57, at least 58, at least 59, at least 60, at least 61, at least 62, at least 63, at least 64, at least 65, at least 66, at least 67, at least 68, at least 69, at least 70, at least 71, at least 72, at least 73, at least 74, at least 75, at least 76, at least 77, at least 78, at least 79, at least 80, at least 81, at least 82, at least 83, at least 84, at least 85, at least 86, at least 87, at least 88, at least 89, at least 90, at least 91, at least 92, at least 93, at least 94, at least 95, at least 96, at least 97, at least 98, at least 99, at least 100, at least 101, at least 102, at least 103, at least 104, at least 105, at least 106, at least 107, at least 108, at least 109, at least 110, at least 111, at least 112, at least 113, at least 114, at least 115, at least 116, at least 117, at least 118, at least 119, at least 120, at least 121, at least 122, at least 123, at least 124, at least 125, at least 126, at least 127, at least 128, at least 129, at least 130, at least 131, at least 132, at least 133, at least 134, at least 135, at least 136, at least 137, at least 138, at least 139, at least 140, at least 141, at least 142, at least 143, at least 144, at least 145, at least 146, at least 147, at least 148, at least 149, at least 150, at least 151, at least 152, at least 153, at least 154, at least 155, at least 156, at least 157, at least 158, at least 159, at least 160, at least 161, at least 162, at least 163, at least 164, at least 165, at least 166, at least 167, at least 168, at least 169, at least 170, at least 171, at least 172, at least 173, at least 174, at least 175, at least 176, at least 177, at least 178, at least 179, at least 180, at least 181, at least 182, at least 183, at least 184, at least 185, at least 186, at least 187, at least 188, at least 189, at least 190, at least 191, at least 192, at least 193, at least 194, at least 195, at least 196, at least 197, at least 198, at least 199, at least 200, at least 201, at least 202, at least 203, at least 204, at least 205, at least 206, at least 207, at least 208, at least 209, at least 210, at least 211, at least 212, at least 213, at least 214, at least 215, at least 216, at least 217, at least 218, at least 219, at least 220, at least 221, at least 222, at least 223, at least 224, at least 225, at least 226, at least 227, at least 228, at least 229, at least 230, at least 231, at least 232, at least 233, at least 234, at least 235, at least 236, at least 237, at least 238, at least 239, at least 240, at least 241, at least 242, at least 243, at least 244, at least 245, at least 246, at least 247, at least 248, at least 249, at least 250, at least 251, at least 252, at least 253, at least 254, at least 255, at least 256, at least 257, at least 258, at least 259, at least 260, at least 261, at least 262, at least 263, at least 264, at least 265, at least 266, at least 267, at least 268, at least 269, at least 270, at least 271, at least 272, at least 273, at least 274, at least 275, at least 276, at least 277, at least 278, at least 279, at least 280, at least 281, at least 282, at least 283, at least 284, at least 285, at least 286, at least 287, at least 288, at least 289, at least 290, at least 291, at least 292, at least 293, at least 294, at least 295,

at least 296, at least 297, at least 298, at least 299, at least 300, at least 301, at least 302, at least 303, at least 304, at least 305, at least 306, at least 307, at least 308, at least 309, at least 310, at least 311, at least 312, at least 313, at least 314, at least 315, at least 316, at least 317, at least 318, at least 319, at least 320, at least 321, at least 322, at least 323, at least 324, at least 325, at least 326, at least 327, at least 328, at least 329, at least 330, at least 331, at least 332, at least 333, at least 334, at least 335, at least 336, at least 337, at least 338, at least 339, at least 340, at least 341, at least 342, at least 343, at least 344, at least 345, at least 346, at least 347, at least 348, at least 349, at least 350, at least 351, at least 352, at least 353, at least 354, at least 355, at least 356, at least 357, at least 358, at least 359, at least 360, at least 361, at least 362, at least 363, at least 364, at least 365, at least 366, at least 367, at least 368, at least 369, at least 370, at least 371, at least 372, at least 373, at least 374, at least 375, at least 376, at least 377, at least 378, at least 379, at least 380, at least 381, at least 382, at least 383, at least 384, at least 385, at least 386, at least 387 consecutive nucleotides in any one of SEQ ID NOs: 20-57. Longer fragments are contemplated, i.e. fragments having at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1500, at least 2000, and at least 2500 nucleotides from those of SEQ ID NOs: 20-57 that encompass fragments of such lengths.

The nucleic acid fragment of the invention discussed above typically has a sequence identity with the nucleotide sequence defined for i) or ii) above, which is at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

The nucleic acid fragment of the invention discussed above may also have a sequence identity with the nucleotide sequence defined for iii) above, which is at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

The Vectors of the Invention

Vectors of the invention fall into several categories discussed infra. One preferred vector of the invention comprises in operable linkage and in the 5'-3' direction, an expression control region comprising an enhancer/promoter for driving expression of the nucleic acid fragment defined for option i) above, optionally a signal peptide coding sequence, a nucleotide sequence defined for option i), and optionally a terminator. Hence, such a vector constitutes an expression vector useful for effecting production in cells of the polypeptide of the invention. Since the polypeptides of the invention are bacterial of origin, recombinant production is conveniently effected in bacterial host cells, so here it is preferred that the expression control region drives expression in prokaryotic cell such as a bacterium, e.g. in *E. coli*. However, if the vector is to drive expression in mammalian cell (as would be the case for a DNA vaccine vector), the expression control region should be adapted to this particular use.

At any rate, certain vectors of the invention are capable of autonomous replication.

Also, the vector of the invention may be one that is capable of being integrated into the genome of a host cell—this is particularly useful if the vector is use in the production of stably transformed cells, where the progeny will also include the genetic information introduced via the

vector. Alternatively, vectors incapable of being integrated into the genome of a mammalian host cell are useful in e.g. DNA vaccination.

Typically, the vector of the invention is selected from the group consisting of a virus, such as an attenuated virus (which may in itself be useful as a vaccine agent), a bacteriophage, a plasmid, a minichromosome, and a cosmid.

A more detailed discussion of vectors of the invention is provided in the following:

Polypeptides of the invention may be encoded by a nucleic acid molecule comprised in a vector. A nucleic acid sequence can be "heterologous," which means that it is in a context foreign to the cell in which the vector is being introduced, which includes a sequence homologous to a sequence in the cell but in a position within the host cell where it is ordinarily not found. Vectors include naked DNAs, RNAs, plasmids, cosmids, viruses (bacteriophage, animal viruses, and plant viruses), and artificial chromosomes (e.g., YACs). One of skill in the art would be well equipped to construct a vector through standard recombinant techniques (for example Sambrook et al, 2001; Ausubel et al, 1996, both incorporated herein by reference). In addition to encoding the polypeptides of this invention, a vector of the present invention may encode polypeptide sequences such as a tag or immunogenicity enhancing peptide (e.g. an immunogenic carrier or a fusion partner that stimulates the immune system, such as a cytokine or active fragment thereof). Useful vectors encoding such fusion proteins include pIN vectors (Inouye et al, 1985), vectors encoding a stretch of histidines, and pGEX vectors, for use in generating glutathione S-transferase (GST) soluble fusion proteins for later purification and separation or cleavage.

Vectors of the invention may be used in a host cell to produce a polypeptide of the invention that may subsequently be purified for administration to a subject or the vector may be purified for direct administration to a subject for expression of the protein in the subject (as is the case when administering a nucleic acid vaccine).

Expression vectors can contain a variety of "control sequences," which refer to nucleic acid sequences necessary for the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well and are described infra.

1. Promoters and Enhancers

A "promoter" is a control sequence. The promoter is typically a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements at which regulatory proteins and molecules may bind such as RNA polymerase and other transcription factors. The phrases "operatively positioned," "operatively linked," "under control," and "under transcriptional control" mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and expression of that sequence. A promoter may or may not be used in conjunction with an "enhancer," which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

A promoter may be one naturally associated with a gene or sequence, as may be obtained by isolating the 5' non-coding sequences located upstream of the coding segment or exon. Such a promoter can be referred to as "endogenous." Similarly, an enhancer may be one naturally associated with a nucleic acid sequence, located either downstream or

upstream of that sequence. Alternatively, certain advantages will be gained by positioning the coding nucleic acid segment under the control of a recombinant or heterologous promoter, which refers to a promoter that is not normally associated with a nucleic acid sequence in its natural environment. A recombinant or heterologous enhancer refers also to an enhancer not normally associated with a nucleic acid sequence in its natural state. Such promoters or enhancers may include promoters or enhancers of other genes, and promoters or enhancers isolated from any other prokaryotic, viral, or eukaryotic cell, and promoters or enhancers not "naturally occurring," i.e., containing different elements of different transcriptional regulatory regions, and/or mutations that alter expression. In addition to producing nucleic acid sequences of promoters and enhancers synthetically, sequences may be produced using recombinant cloning and/or nucleic acid amplification technology, including PCR™, in connection with the compositions disclosed herein (see U.S. Pat. No. 4,683,202, U.S. Pat. No. 5,928,906, each incorporated herein by reference).

Naturally, it may be important to employ a promoter and/or enhancer that effectively direct(s) the expression of the DNA segment in the cell type or organism chosen for expression. Those of skill in the art of molecular biology generally know the use of promoters, enhancers, and cell type combinations for protein expression (see Sambrook et al, 2001, incorporated herein by reference). The promoters employed may be constitutive, tissue-specific, or inducible and in certain embodiments may direct high level expression of the introduced DNA segment under specified conditions, such as large-scale production of recombinant proteins or peptides.

Examples of inducible elements, which are regions of a nucleic acid sequence that can be activated in response to a specific stimulus, include but are not limited to Immunoglobulin Heavy Chain (Banerji et al, 1983; Gilles et al, 1983; Grosschedl et al, 1985; Atchinson et al, 1986, 1987; toiler et al, 1987; Weinberger et al, 1984; Kiledjian et al, 1988; Porton et al; 1990), Immunoglobulin Light Chain (Queen et al, 1983; Picard et al, 1984), T Cell Receptor (Luria et al, 1987; Winoto et al, 1989; Redondo et al; 1990), HLA DQ α and/or DQ β (Sullivan et al, 1987), β -Interferon (Goodbourn et al, 1986; Fujita et al, 1987; Goodbourn et al, 1988), Interleukin-2 (Greene et al, 1989), Interleukin-2 Receptor (Greene et al, 1989; Lin et al, 1990), MHC Class II 5 (Koch et al, 1989), MHC Class II HLA-DR α (Sherman et al, 1989), β -Actin (Kawamoto et al, 1988; Ng et al; 1989), Muscle Creatine Kinase (MCK) (Jaynes et al, 1988; Horlick et al, 1989; Johnson et al, 1989), Prealbumin (Transthyretin) (Costa et al, 1988), Elastase I (Omitz et al, 1987), Metallothionein (MTII) (Karin et al, 1987; Culotta et al, 1989), Collagenase (Pinkert et al, 1987; Angel et al, 1987), Albumin (Pinkert et al, 1987; Tranche et al, 1989, 1990), α -Fetoprotein (Godbout et al, 1988; Campere et al, 1989), γ -Globin (Bodine et al, 1987; Perez-Stable et al, 1990), β -Globin (Trudel et al, 1987), c-fos (Cohen et al, 1987), c-HA-ras (Triesman, 1986; Deschamps et al, 1985), Insulin (Edlund et al, 1985), Neural Cell Adhesion Molecule (NCAM) (Hirsh et al, 1990), α 1-Antitrypsin (Larimer et al, 1990), H2B (TH2B) Histone (Hwang et al, 1990), Mouse and/or Type I Collagen (Ripe et al, 1989), Glucose-Regulated Proteins (GRP94 and GRP78) (Chang et al, 1989), Rat Growth Hormone (Larsen et al, 1986), Human Serum Amyloid A (SAA) (Edbrooke et al, 1989), Troponin I (TN I) (Yutzey et al, 1989), Platelet-Derived Growth Factor (PDGF) (Pech et al, 1989), Duchenne Muscular Dystrophy (Klamut et al, 1990), SV40 (Banerji et al, 1981; Moreau et

al, 1981; Sleight et al, 1985; Firak et al, 1986; Herr et al, 1986; Imbra et al, 1986; Kadesch et al, 1986; Wang et al, 1986; Ondek et al, 1987; Kuhl et al, 1987; Schaffner et al, 1988), Polyoma (Swartzendruber et al, 1975; Vasseur et al, 1980; Katinka et al, 1980, 1981; Tyndell et al, 1981; Dandolo et al, 1983; de Villiers et al, 1984; Hen et al, 1986; Satake et al, 1988; Campbell et al, 1988), Retroviruses (Kriegler et al, 1982, 1983; Levinson et al, 1982; Kriegler et al, 1983, 1984a, b, 1988; Bosze et al, 1986; Miksicek et al, 1986; Celander et al, 1987; Thiesen et al, 1988; Celander et al, 1988; Choi et al, 1988; Reisman et al, 1989), Papilloma Virus (Campo et al, 1983; Lusky et al, 1983; Spandidos and Wilkie, 1983; Spalholz et al, 1985; Lusky et al, 1986; Cripe et al, 1987; Gloss et al, 1987; Hirochika et al, 1987; Stephens et al, 1987), Hepatitis B Virus (Bulla et al, 1986; Jameel et al, 1986; Shaul et al, 1987; Spandau et al, 1988; Vannice et al, 1988), Human Immunodeficiency Virus (Muesing et al, 1987; Hauber et al, 1988; Jakobovits et al, 1988; Feng et al, 1988; Takebe et al, 1988; Rosen et al, 1988; Berkhout et al, 1989; Laspia et al, 1989; Sharp et al, 1989; Braddock et al, 1989), Cytomegalovirus (CMV) IE (Weber et al, 1984; Boshart et al, 1985; Foecking et al, 1986), Gibbon Ape Leukemia Virus (Holbrook et al, 1987; Quinn et al, 1989).

Inducible Elements include, but are not limited to MT II—Phorbol Ester (TFA)/Heavy metals (Palmiter et al, 1982; Haslinger et al, 1985; Searle et al, 1985; Stuart et al, 1985; Imagawa et al, 1987; Karin et al, 1987; Angel et al, 1987b; McNeall et al, 1989); MMTV (mouse mammary tumor virus)—Glucocorticoids (Huang et al, 1981; Lee et al, 1981; Majors et al, 1983; Chandler et al, 1983; Lee et al, 1984; Ponta et al, 1985; Sakai et al, 1988); β -Interferon—poly(rI) x/poly(rc) (Tavernier et al, 1983); Adenovirus 5 E2—E1A (Imperiale et al, 1984); Collagenase—Phorbol Ester (TPA) (Angel et al, 1987a); Stromelysin—Phorbol Ester (TPA) (Angel et al, 1987b); SV40—Phorbol Ester (TPA) (Angel et al, 1987b); Murine MX Gene—Interferon, Newcastle Disease Virus (Hug et al, 1988); GRP78 Gene—A23187 (Resendez et al, 1988); α -2-Macroglobulin—IL-6 (Kunz et al, 1989); Vimentin—Serum (Rittling et al, 1989); MHC Class I Gene H-2kb—Interferon (Blonar et al, 1989); HSP70—E1A/SV40 Large T Antigen (Taylor et al, 1989, 1990a, 1990b); Proliferin—Phorbol Ester/TPA (Mordacq et al, 1989); Tumor Necrosis Factor—PMA (Hensel et al, 1989); and Thyroid Stimulating Hormone Gene—Thyroid Hormone (Chatterjee et al, 1989).

Also contemplated as useful in the present invention are the dectin-1 and dectin-2 promoters. Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of structural genes encoding oligosaccharide processing enzymes, protein folding accessory proteins, selectable marker proteins or a heterologous protein of interest.

The particular promoter that is employed to control the expression of peptide or protein encoding polynucleotide of the invention is not believed to be critical, so long as it is capable of expressing the polynucleotide in a targeted cell, preferably a bacterial cell. Where a human cell is targeted, it is preferable to position the polynucleotide coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell. Generally speaking, such a promoter might include either a bacterial, human or viral promoter.

In various embodiments, the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter, and the Rous sarcoma virus long terminal repeat can be used to obtain high level expression of a related polynucleotide to this invention. The use of other viral or

mammalian cellular or bacterial phage promoters, which are well known in the art, to achieve expression of polynucleotides is contemplated as well.

In embodiments in which a vector is administered to a subject for expression of the protein, it is contemplated that a desirable promoter for use with the vector is one that is not down-regulated by cytokines or one that is strong enough that even if down-regulated, it produces an effective amount of the protein/polypeptide of the current invention in a subject to elicit an immune response. Non-limiting examples of these are CMV IE and RSV LTR. In other embodiments, a promoter that is up-regulated in the presence of cytokines is employed. The MHC I promoter increases expression in the presence of IFN- γ .

Tissue specific promoters can be used, particularly if expression is in cells in which expression of an antigen is desirable, such as dendritic cells or macrophages. The mammalian MHC I and MHC II promoters are examples of such tissue-specific promoters. 2. Initiation Signals and Internal Ribosome Binding Sites (IRES)

A specific initiation signal also may be required for efficient translation of coding sequences. These signals include the ATG initiation codon or adjacent sequences. Exogenous translational control signals, including the ATG initiation codon, may need to be provided. One of ordinary skill in the art would readily be capable of determining this and providing the necessary signals. It is well known that the initiation codon must be "in-frame" with the reading frame of the desired coding sequence to ensure translation of the entire insert. The exogenous translational control signals and initiation codons can be either natural or synthetic and may be operable in bacteria or mammalian cells. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements.

In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5' methylated Cap dependent translation and begin translation at internal sites (Pelletier and Sonenberg, 1988). IRES elements from two members of the picornavirus family (polio and encephalomyocarditis) have been described (Pelletier and Sonenberg, 1988), as well as an IRES from a mammalian message (Macejak and Sarnow, 1991). IRES elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each separated by an IRES, creating polycistronic messages. By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation. Multiple genes can be efficiently expressed using a single promoter/enhancer to transcribe a single message (see U.S. Pat. Nos. 5,925,565 and 5,935,819, herein incorporated by reference).

2. Multiple Cloning Sites

Vectors can include a multiple cloning site (MCS), which is a nucleic acid region that contains multiple restriction enzyme sites, any of which can be used in conjunction with standard recombinant technology to digest the vector. (See Carbonelli et al, 1999, Levenson et al, 1998, and Cocea, 1997, incorporated herein by reference.) Frequently, a vector is linearized or fragmented using a restriction enzyme that cuts within the MCS to enable exogenous sequences to be ligated to the vector. Techniques involving restriction enzymes and ligation reactions are well known to those of skill in the art of recombinant technology.

3. Splicing Sites

Most transcribed eukaryotic RNA molecules will undergo RNA splicing to remove introns from the primary tran-

scripts. If relevant in the context of vectors of the present invention, vectors containing genomic eukaryotic sequences may require donor and/or acceptor splicing sites to ensure proper processing of the transcript for protein expression. (See Chandler et al, 1997, incorporated herein by reference.)

4. Termination Signals

The vectors or constructs of the present invention will generally comprise at least one termination signal. A "termination signal" or "terminator" is comprised of the DNA sequences involved in specific termination of an RNA transcript by an RNA polymerase. Thus, in certain embodiments a termination signal that ends the production of an RNA transcript is contemplated. A terminator may be necessary in vivo to achieve desirable message levels.

In eukaryotic systems, the terminator region may also comprise specific DNA sequences that permit site-specific cleavage of the new transcript so as to expose a polyadenylation site. This signals a specialized endogenous polymerase to add a stretch of about 200 A residues (poly A) to the 3' end of the transcript. RNA molecules modified with this polyA tail appear to more stable and are translated more efficiently. Thus, in other embodiments involving eukaryotes, it is preferred that that terminator comprises a signal for the cleavage of the RNA, and it is more preferred that the terminator signal promotes polyadenylation of the message.

Terminators contemplated for use in the invention include any known terminator of transcription described herein or known to one of ordinary skill in the art, including but not limited to, for example, the bovine growth hormone terminator or viral termination sequences, such as the SV40 terminator. In certain embodiments, the termination signal may be a lack of transcribable or translatable sequence, such as due to a sequence truncation.

5. Polyadenylation Signals

In expression, particularly eukaryotic expression (as is relevant in nucleic acid vaccination), one will typically include a polyadenylation signal to effect proper polyadenylation of the transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and/or any such sequence may be employed. Preferred embodiments include the SV40 polyadenylation signal and/or the bovine growth hormone polyadenylation signal, convenient and/or known to function well in various target cells.

Polyadenylation may increase the stability of the transcript or may facilitate cytoplasmic transport.

6. Origins of Replication

In order to propagate a vector in a host cell, it may contain one or more origins of replication sites (often termed "on"), which is a specific nucleic acid sequence at which replication is initiated. Alternatively an autonomously replicating sequence (ARS) can be employed if the host cell is yeast.

7. Selectable and Screenable Markers

In certain embodiments of the invention, cells containing a nucleic acid construct of the present invention may be identified in vitro or in vivo by encoding a screenable or selectable marker in the expression vector. When transcribed and translated, a marker confers an identifiable change to the cell permitting easy identification of cells containing the expression vector. Generally, a selectable marker is one that confers a property that allows for selection. A positive selectable marker is one in which the presence of the marker allows for its selection, while a negative selectable marker is one in which its presence prevents its selection. An example of a positive selectable marker is a drug resistance marker.

Usually the inclusion of a drug selection marker aids in the cloning and identification of transformants, for example, markers that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin or histidinol are useful selectable markers. In addition to markers conferring a phenotype that allows for the discrimination of transformants based on the implementation of conditions, other types of markers including screenable markers such as GFP for colorimetric analysis. Alternatively, screenable enzymes such as herpes simplex virus thymidine kinase (tk) or chloramphenicol acetyltransferase (CAT) may be utilized. One of skill in the art would also know how to employ immunologic markers that can be used in conjunction with FACS analysis. The marker used is not believed to be important, so long as it is capable of being expressed simultaneously with the nucleic acid encoding a protein of the invention. Further examples of selectable and screenable markers are well known to one of skill in the art.

The Transformed Cells of the Invention

Transformed cells of the invention are useful as organisms for producing the polypeptide of the invention, but also as simple "containers" of nucleic acids and vectors of the invention.

Certain transformed cells of the invention are capable of replicating the nucleic acid fragment defined for option i) of the second aspect of the invention. Preferred transformed cells of the invention are capable of expressing the nucleic acid fragment defined for option i).

For recombinant production it is convenient, but not a prerequisite that the transformed cell according is prokaryotic, such as a bacterium, but generally both prokaryotic cells and eukaryotic cells may be used.

Suitable prokaryotic cells are bacterial cells selected from the group consisting of *Escherichia* (such as *E. coli*), *Bacillus* [e.g. *Bacillus subtilis*], *Salmonella*, and *Mycobacterium* [preferably non-pathogenic, e.g. *M. bovis* BCG].

Eukaryotic cells can be in the form of yeasts (such as *Saccharomyces cerevisiae*) and protozoans. Alternatively, the transformed eukaryotic cells are derived from a multicellular organism such as a fungus, an insect cell, a plant cell, or a mammalian cell.

For production purposes, it is advantageous that the transformed cell of the invention is stably transformed by having the nucleic acid defined above for option i) stably integrated into its genome, and in certain embodiments it is also preferred that the transformed cell secretes or carries on its surface the polypeptide of the invention, since this facilitates recovery of the polypeptides produced. A particular version of this embodiment is one where the transformed cell is a bacterium and secretion of the polypeptide of the invention is into the periplasmic space.

As noted above, stably transformed cells are preferred—these inter alia (i.a.) allows that cell lines comprised of transformed cells as defined herein may be established—such cell lines are particularly preferred aspects of the invention.

Further details on cells and cell lines are presented in the following:

Suitable cells for recombinant nucleic acid expression of the nucleic acid fragments of the present invention are prokaryotes and eukaryotes. Examples of prokaryotic cells include *E. coli*; members of the *Staphylococcus* genus, such as *S. epidermidis*; members of the *Lactobacillus* genus, such as *L. plantarum*; members of the *Lactococcus* genus, such as *L. lactis*; members of the *Bacillus* genus, such as *B. subtilis*; members of the *Corynebacterium* genus such as *C. glutamicum*; and members of the *Pseudomonas* genus such as *Ps.*

fluorescens. Examples of eukaryotic cells include mammalian cells; insect cells; yeast cells such as members of the *Saccharomyces* genus (e.g. *S. cerevisiae*), members of the *Pichia* genus (e.g. *P. pastoris*), members of the *Hansenula* genus (e.g. *H. polymorpha*), members of the *Kluyveromyces* genus (e.g. *K. lactis* or *K. fragilis*) and members of the *Schizosaccharomyces* genus (e.g. *S. pombe*).

Techniques for recombinant gene production, introduction into a cell, and recombinant gene expression are well known in the art. Examples of such techniques are provided in references such as Ausubel, Current Protocols in Molecular Biology, John Wiley, 1987-2002, and Sambrook et al., Molecular Cloning, A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989.

As used herein, the terms “cell,” “cell line,” and “cell culture” may be used interchangeably. All of these terms also include their progeny, which is any and all subsequent generations. It is understood that all progeny may not be identical due to deliberate or inadvertent mutations. In the context of expressing a heterologous nucleic acid sequence, “host cell” refers to a prokaryotic or eukaryotic cell, and it includes any transformable organism that is capable of replicating a vector or expressing a heterologous gene encoded by a vector. A host cell can, and has been, used as a recipient for vectors or viruses. A host cell may be “transfected” or “transformed,” which refers to a process by which exogenous nucleic acid, such as a recombinant protein-encoding sequence, is transferred or introduced into the host cell. A transformed cell includes the primary subject cell and its progeny.

Host cells may be derived from prokaryotes or eukaryotes, including bacteria, yeast cells, insect cells, and mammalian cells for replication of the vector or expression of part or all of the nucleic acid sequence(s). Numerous cell lines and cultures are available for use as a host cell, and they can be obtained through the American Type Culture Collection (ATCC), which is an organization that serves as an archive for living cultures and genetic materials (www.atcc.org) or from other depository institutions such as Deutsche Sammlung vor Mikroorganismen und Zellkulturen (DSMZ). An appropriate host can be determined by one of skill in the art based on the vector backbone and the desired result. A plasmid or cosmid, for example, can be introduced into a prokaryote host cell for replication of many vectors or expression of encoded proteins. Bacterial cells used as host cells for vector replication and/or expression include *Staphylococcus* strains, DH5a, JMI 09, and KC8, as well as a number of commercially available bacterial hosts such as SURE[®] Competent Cells and SOLOP ACK[™] Gold Cells (STRATAGENE[®], La Jolla, Calif.). Alternatively, bacterial cells such as *E. coli* LE392 could be used as host cells for phage viruses. Appropriate yeast cells include *Saccharomyces cerevisiae*, *Saccharomyces pombe*, and *Pichia pastoris*.

Examples of eukaryotic host cells for replication and/or expression of a vector include HeLa, NIH3T3, Jurkat, 293, Cos, CHO, Saos, and PC12. Many host cells from various cell types and organisms are available and would be known to one of skill in the art. Similarly, a viral vector may be used in conjunction with either a eukaryotic or prokaryotic host cell, particularly one that is permissive for replication or expression of the vector.

Some vectors may employ control sequences that allow it to be replicated and/or expressed in both prokaryotic and eukaryotic cells. One of skill in the art would further understand the conditions under which to incubate all of the above described host cells to maintain them and to permit

replication of a vector. Also understood and known are techniques and conditions that would allow large-scale production of vectors, as well as production of the nucleic acids encoded by vectors and their cognate polypeptides, proteins, or peptides.

Expression Systems

Numerous expression systems exist that comprise at least a part or all of the compositions discussed above. Prokaryote- and/or eukaryote-based systems can be employed for use with the present invention to produce nucleic acid sequences, or their cognate polypeptides, proteins and peptides. Many such systems are commercially and widely available.

The insect cell/baculovirus system can produce a high level of protein expression of a heterologous nucleic acid segment, such as described in U.S. Pat. Nos. 5,871,986, 4,879,236, both herein incorporated by reference, and which can be bought, for example, under the name MAXBAC[®] 2.0 from INVITROGEN[®] and BACPACK[™] Baculovirus expression system from CLONTECH[®].

In addition to the disclosed expression systems of the invention, other examples of expression systems include STRATAGENE[®]'s COMPLETE CONTROL[™] Inducible Mammalian Expression System, which involves a synthetic ecdysone-inducible receptor, or its pET Expression System, an *E. coli* expression system. Another example of an inducible expression system is available from INVITROGEN[®], which carries the T-REX[™] (tetracycline-regulated expression) System, an inducible mammalian expression system that uses the full-length CMV promoter. INVITROGEN[®] also provides a yeast expression system called the *Pichia methanolica* Expression System, which is designed for high-level production of recombinant proteins in the methylophilic yeast *Pichia methanolica*. One of skill in the art would know how to express a vector, such as an expression construct, to produce a nucleic acid sequence or its cognate polypeptide, protein, or peptide.

Amplification of Nucleic Acids

Nucleic acids used as a template for amplification may be isolated from cells, tissues or other samples according to standard methodologies (Sambrook et al, 2001). In certain embodiments, analysis is performed on whole cell or tissue homogenates or biological fluid samples without substantial purification of the template nucleic acid. The nucleic acid may be genomic DNA or fractionated or whole cell RNA. Where RNA is used, it may be desired to first convert the RNA to a complementary DNA.

The term “primer,” as used herein, is meant to encompass any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent process. Typically, primers are oligonucleotides from ten to twenty and/or thirty base pairs in length, but longer sequences can be employed. Primers may be provided in double-stranded and/or single-stranded form, although the single-stranded form is preferred.

Pairs of primers designed to selectively hybridize to nucleic acids corresponding to sequences of genes identified herein are contacted with the template nucleic acid under conditions that permit selective hybridization. Depending upon the desired application, high stringency hybridization conditions may be selected that will only allow hybridization to sequences that are completely complementary to the primers. In other embodiments, hybridization may occur under reduced stringency to allow for amplification of nucleic acids containing one or more mismatches with the primer sequences. Once hybridized, the template-primer complex is contacted with one or more enzymes that facili-

tate template-dependent nucleic acid synthesis. Multiple rounds of amplification, also referred to as "cycles," are conducted until a sufficient amount of amplification product is produced.

The amplification product may be detected or quantified. In certain applications, the detection may be performed by visual means. Alternatively, the detection may involve indirect identification of the product via chemiluminescence, radioactive scintigraphy of incorporated radiolabel or fluorescent label or even via a system using electrical and/or thermal impulse signals (Bellus, 1994).

A number of template dependent processes are available to amplify the oligonucleotide sequences present in a given template sample. One of the best known amplification methods is the polymerase chain reaction (referred to as PCR™) which is described in detail in U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,800,159, and in Innis et al., 1988, each of which is incorporated herein by reference in their entirety.

Alternative methods for amplification of target nucleic acid sequences that may be used in the practice of the present invention are disclosed in U.S. Pat. Nos. 5,843,650, 5,846,709, 5,846,783, 5,849,546, 5,849,497, 5,849,547, 5,858,652, 5,866,366, 5,916,776, 5,922,574, 5,928,905, 5,928,906, 5,932,451, 5,935,825, 5,939,291 and 5,942,391, GB Application No. 2 202 328, and in PCT Application No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety.

Methods of Gene Transfer

Suitable methods for nucleic acid delivery to effect expression of compositions of the present invention are believed to include virtually any method by which a nucleic acid (e.g., DNA, including viral and nonviral vectors) can be introduced into a cell, a tissue or an organism, as described herein or as would be known to one of ordinary skill in the art. Such methods include, but are not limited to, direct delivery of DNA such as by injection (U.S. Pat. Nos. 5,994,624, 5,981,274, 5,945,100, 5,780,448, 5,736,524, 5,702,932, 5,656,610, 5,589,466 and 5,580,859, each incorporated herein by reference), including microinjection (Harland and Weintraub, 1985; U.S. Pat. No. 5,789,215, incorporated herein by reference); by electroporation (U.S. Pat. No. 5,384,253, incorporated herein by reference); by calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe et al., 1990); by using DEAE dextran followed by polyethylene glycol (Gopal, 1985); by direct sonic loading (Fechheimer et al, 1987); by liposome mediated transfection (Nicolau and Sene, 1982; Fraley et al, 1979; Nicolau et al, 1987; Wong et al, 1980; Kaneda et al, 1989; Kato et al, 1991); by microprojectile bombardment (PCT Application Nos. WO 94/09699 and 95/06128; U.S. Pat. Nos. 5,610,042; 5,322,783 5,563,055, 5,550,318, 5,538,877 and 5,538,880, and each incorporated herein by reference); by agitation with silicon carbide fibers (Kaeppler et al, 1990; U.S. Pat. Nos. 5,302,523 and 5,464,765, each incorporated herein by reference); by *Agrobacterium* mediated transformation (U.S. Pat. Nos. 5,591,616 and 5,563,055, each incorporated herein by reference); or by PEG mediated transformation of protoplasts (Omirulleh et al, 1993; U.S. Pat. Nos. 4,684,611 and 4,952,500, each incorporated herein by reference); by desiccation/inhibition mediated DNA uptake (Potrykus et al, 1985). Through the application of techniques such as these, organelle(s), cell(s), tissue(s) or organism(s) may be stably or transiently transformed.

The Antibodies of the Invention—and their Production/ Isolation

Antibodies directed against the proteins of the invention are useful for affinity chromatography, immunoassays, and for distinguishing/identifying *staphylococcus* proteins as well as for passive immunisation and therapy.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by in vitro immunization using methods known in the art, which for the purposes of this invention is considered equivalent to in vivo immunization. Polyclonal antiserum is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25 C for one hour, followed by incubating at 4 C for 2-18 hours. The serum is recovered by centrifugation (e.g. 1,000 g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein [Nature (1975) 256: 495-96], or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells expressing membrane-bound immunoglobulin specific for the antigen bind to the plate, and are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g. hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for production of antibodies, which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either in vitro (e.g. in tissue culture bottles or hollow fiber reactors), or in vivo (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ³²P and ¹²⁵I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3', 5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same

label may serve in several different modes. For example, 1151 may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAB. Further, one may combine various labels for desired effect. For example, MABs and avidin also require labels in the practice of this invention: thus, one might label a MAB with biotin, and detect its presence with avidin labeled with, 125I, or with an anti-biotin MAB labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

According to the invention, the isolated monoclonal antibody or antibody analogue is preferably a monoclonal antibody selected from a multi-domain antibody such as a murine antibody, a chimeric antibody such as a humanized antibody, a fully human antibody, and single-domain antibody of a llama or a camel, or which is an antibody analogue selected from a fragment of an antibody such as an Fab or an F(ab')₂, an scFV; cf. also the definition of the term "antibody" presented above.

Compositions of the Invention; Vaccines

Pharmaceutical compositions, in particular vaccines, according to the invention may either be prophylactic (i.e. to prevent infection) or therapeutic (i.e. to treat disease after infection).

Such vaccines comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid(s), usually in combination with "pharmaceutically acceptable carriers", which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles.

Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogen, cf. the description of immunogenic carriers supra.

The pharmaceutical compositions of the invention thus typically contain an immunological adjuvant, which is commonly an aluminium based adjuvant or one of the other adjuvants described in the following:

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (WO 90/14837; Chapter 10 in Vaccine design: the subunit and adjuvant approach, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, Mass.), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi adjuvant system (RAS), (Ribi Immunochem, Hamilton, Mont.) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of

monophosphoryl lipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL+CWS (Detox™); (3) saponin adjuvants such as Stimulon™ (Cambridge Bioscience, Worcester, Mass.) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g. gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc.; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ adjuvants are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2"-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The immunogenic compositions (e.g. the immunising antigen or immunogen or polypeptide or protein or nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g. nonhuman primate, primate, etc.), the capacity of the individual's immune system to synthesize antibodies or generally mount an immune response, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials. However, for the purposes of protein vaccination, the amount administered per immunization is typically in the range between 0.5 µg and 500 mg (however, often not higher than 5,000 µg), and very often in the range between 10 and 200 µg.

The immunogenic compositions are conventionally administered parenterally, e.g. by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (e.g. WO98/20734). Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. In the case of nucleic acid vaccination, also the intravenous or intraarterial routes may be applicable.

Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination (also termed nucleic acid vaccination or gene vacci-

nation) may be used [e.g. Robinson & Torres (1997) Seminars in Immunol 9: 271-283; Donnelly et al. (1997) Avnu Rev Immunol 15: 617-648; later herein].

Treatment Methods of the Invention

The method of the sixth aspect of the invention generally relates to induction of immunity and as such also entails method that relate to treatment, prophylaxis and amelioration of disease.

When immunization methods entail that a polypeptide of the invention or a composition comprising such a polypeptide is administered the animal (e.g. the human) typically receives between 0.5 and 5,000 µg of the polypeptide of the invention per administration.

In preferred embodiments of the sixth aspect, the immunization scheme includes that the animal (e.g. the human) receives a priming administration and one or more booster administrations.

Preferred embodiments of the 6th aspect of the invention comprise that the administration is for the purpose of inducing protective immunity against *S. aureus*. In this embodiment it is particularly preferred that the protective immunity is effective in reducing the risk of attracting infection with *S. aureus* or is effective in treating or ameliorating infection with *S. aureus*.

As mention herein, the preferred vaccines of the invention induce humoral immunity, so it is preferred that the administration is for the purpose of inducing antibodies specific for *S. aureus* and wherein said antibodies or B-lymphocytes producing said antibodies are subsequently recovered from the animal.

But, as also mentioned the method of the 6th aspect may also be useful in antibody production, so in other embodiments the administration is for the purpose of inducing antibodies specific for *S. aureus* and wherein B-lymphocytes producing said antibodies are subsequently recovered from the animal and used for preparation of monoclonal antibodies.

Pharmaceutical compositions can as mentioned above comprise polypeptides, antibodies, or nucleic acids of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount thereof.

The term "therapeutically effective amount" or "prophylactically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. Reference is however made to the ranges for dosages of immunologically effective amounts of polypeptides, cf. above.

However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide,

genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

As is apparent from the claim, the invention also relates to related embodiments to the treatment and prophylaxis disclosed herein: the invention also includes embodiments where

the polypeptide of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *S. aureus*;

the nucleic acid fragment of the invention or the vector of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *S. aureus*;

the transformed cell of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *S. aureus*.

the antibody, antibody fragment or antibody analogue of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *S. aureus*.

EXAMPLE

Protocol for Testing *S. aureus* Derived Vaccines in Mice

Expression and Purification of *S. aureus* Genes

1. Gene fragments that encode the selected *S. aureus* polypeptides of the invention are prepared synthetically and are introduced into the pQE-1 vector (Qiagen) from GenScript. The fragments are inserted by blunt ended ligation into the PVU II site in the 5'-end, immediately following the vector's coding region for the 6 histidinyl residues. In the 3'-end, all inserted gene fragments include a stop codon.

2. The vectors from 1 are transfected into the *E. Coli* M15[pREP4] strain, which contains an expression as well as a repressor plasmid facilitating proper expression.

3. The vectors from 1 are further inserted into the *E. coli* XL1 Blue for long-time storage.

4. The transfected and selected clones are tested for expression in small scale whereby optimum conditions for

expression in terms of the amount of IPTG, the density of cells and the time of expression induction are determined.

5. From the information obtained in 4, large scale cultures are established; subsequently the expression products are harvested and purified on a Ni-NTA column.

6. Purity and yield of the large-scale expression is investigated by means of SDS-PAGE and spectrophotometry, whereafter the proteins are aliquoted for use in immunization experiments and other experiments.

Immunization and *S. aureus* Challenge Infection in Mice (Zhou et al. 2006 Vaccine 24. 4830-4837)

1. 2 months old NMRI mice were used.

2. Groups of 8 mice (unless other numbers are indicated) were used for immunization. The mice were immunized 3 times (at day 0, 14, and 28) prior to challenge infection. A control group of 8 mice was treated according to an identical protocol with the exception that an irrelevant protein antigen was used for immunization.

1st Immunization:

50 µg protein (per mice) was mixed with 100 µl aluminum hydroxide (Alhydrogel 2.0%, Brenntag) per 125 µg protein and incubated with end-over-end rotation for 15 min. Freund's incomplete adjuvant (sigma) was added in the volume 1:1 and the mixture was vortexed thoroughly for 1 hour. This mixture was injected subcutaneously

2nd and 3rd Immunization

The mice were booster injected intraperitoneally with 2 weeks interval, using the same amount of protein mixed with aluminum hydroxide and physiological saline solution.

3. One week after the last immunization 250 µl blood is drawn from the mice in order to determine the antibody titer.

4. 14 days after the last immunization, a number of bacteria (2×10^9 cells) corresponding to a predetermined LD₅₀ in the control group of mice was administered intraperitoneally to all mice.

The cells were handled cold and kept on ice until use. The stock solution of MRSA cells were thawed on ice and then the appropriate amount of cells in sterile physiological saline (total volume per mouse 500 µl).

The survival was surveilled twice daily in the first 48 hours after challenge and once daily in the subsequent 7 days. The mice were sacrificed if they showed signs of suffering. The mice were monitored with respect to loss of weight and body temperature using an implanted chip. The organs of the mice were used for determination of CFU counts.

Test of Antibody Titer

Maxisorp microtiter plates (Nunc, Roskilde, Denmark) were coated overnight with 1 µg/ml recombinant peptide (His-tagged SAR-protein), 100 µl/well.

The next day the plates were emptied and washed 3 times in PBS-Tw. After the last wash the plates were allowed to stand in PBS-Tw for a minimum of 15 minutes (blocking step).

EDTA plasma was diluted 1:100 in PBS-Tw and 200 µl was added to the first well. 100 µl of washing buffer was added to all of the other wells.

A 2-fold dilution was made by transferring 100 µl from the first well to the next, and so on. The plates were incubated at room temperature for 2 hours with shaking.

The plates were washed and 100 µl of secondary antibody was added per well (e.g. HRP conjugated polyclonal rabbit anti-mouse immunoglobulin) and then incubated for 1 hour at room temperature with shaking.

The plates were washed and the ELISA developed.

The optical density value was used to calculate the antibody titer: [1/Dilution at 1/2 max absorbance].

Buffers used were:

Coating buffer: 15 mM Na₂CO₃, 35 mM NaHCO₃

PBS-Tw: PBS, 0.05% Tween-20 pH 7.4

Coloring buffer for developing the ELISA: 7.3 g citric acid, 11.86 g NaHPO₄ pH 5.0 at 1 L. OPD tablets (KemEn-Tec, Diagnostic) were added, 2 mg per 5 ml coloring buffer. Immediately before use, 2 ml of 35% H₂O₂ was added per tablet. 100 ml of the mixed coloring substrate was added to each well. The reaction was stopped with 100 ml 1M H₂SO₄.

Result of Challenge Studies

The polypeptides used in the challenge studies described are in the following section setting forth the results provided with identification numbers in the format "SARXXXX". For easy reference, these polypeptides relate to the SEQ ID NOs used herein according to the following table:

| | | | |
|------------|---------|------------|---------|
| SEQ ID 1: | SAR2104 | SEQ ID 2: | SAR1879 |
| SEQ ID 3: | SAR0730 | SEQ ID 4: | SAR2722 |
| SEQ ID 5: | SAR1507 | SEQ ID 6: | SAR0222 |
| SEQ ID 7: | SAR1558 | SEQ ID 8: | SAR1026 |
| SEQ ID 9: | SAR1489 | SEQ ID 10: | SAR1819 |
| SEQ ID 11: | SAR0826 | SEQ ID 12: | SAR0390 |
| SEQ ID 13: | SAR0280 | SEQ ID 14: | SAR1816 |
| SEQ ID 15: | SAR0992 | SEQ ID 16: | SAR1881 |
| SEQ ID 17: | SAR0735 | SEQ ID 18: | SAR2119 |
| SEQ ID 19: | SAR2184 | | |

The challenge study gave the following results in term of overall survival in the vaccinated groups vs. the control groups:

| Vaccine protein | Percentage of mice surviving at end of experiment | |
|---|---|-----------------------|
| | Vaccinated mice | Control control group |
| SAR2104-20-154 | 50% | 0% |
| SAR0280-28-820 | 75% | 0% |
| SAR0390-21-190 | 0% | 0% |
| SAR2104-20-154 | 25% | 0%* |
| SAR1879-24-184 | 14%* | 0%* |
| SAR0222-27-609 | 13% | 0%* |
| SAR1881-25-208 | 13% | 0%* |
| SAR2119-34-370 | 25% | 0%* |
| SAR0872-27-273 | 29%* | 0%* |
| SAR2718-24-157 | 17%** | 0%* |
| SAR1816-1-27 | 67%** | 0% |
| | | (50%) |
| SAR0735-26-227 | 88% | 0% |
| | | (50%) |
| SAR0992-428-769 | 29%* | 0% |
| | | (50%) |
| SAR1816-46-396 | 63% | 0% |
| | | (50%) |
| 1:1:1 Mixture of SAR2104-20-154 SAR0280-28-820 SAR0872-27-273 | 88%# | 0%# |
| SAR0826-42-209 | 0% | (13%) |
| SAR0992-1-409 | 100% | (13%) |
| SAR1489-343-486 | 75% | (13%) |
| SAR1507-1-652 | 88% | (13%) |
| SAR1558-21-144 | 38% | (10%) |
| SAR0730-22-129 | 100%* | (13%) |
| SAR1819-1-1274 | 88% | (13%) |
| SAR2722-920-948 | 63% | (13%) |
| SAR1972-23-91 | 50% | (13%) |
| SAR2104-20-154_nativ | 63% | (13%) |
| SAR0280-28-820_nativ | 63% | (13%) |

*7 mice in group

**6 mice in group

#16 mice in group

Percentages in parentheses in control group column indicate survival rate in control group, where mice received injection with adjuvant mixture. Percentages without parentheses in control group column indicate survival rate in control group, where mice received saline only.

Results of ELISA Tests

The tables set forth on the following pages show the OD measurements and, where applicable, in vaccinated mice from the different treatment groups:

| Test protein: SAR 2104-20-154 | | | | | | | | | | | | | | |
|-------------------------------|-------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID | No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| Juni 2104 | 18 | 3 | 4 | 4 | 4 | 3.777 | 3.441 | 2.735 | 1.958 | 1.293 | 0.733 | 0.428 | 0.246 | 0.12 |
| Juni 2104 | 20 | 3 | 4 | 4 | 4 | 4 | 3.789 | 3.282 | 2.436 | 1.6 | 0.979 | 0.547 | 0.262 | 0.121 |
| Juni 2104 | 22 | 3 | 3.894 | 3.892 | 3.897 | 3.871 | 3.544 | 3.122 | 2.573 | 2.006 | 1.383 | 0.841 | 0.481 | 0.252 |
| Juni 2104 | 24 | 3 | 4 | 4 | 4 | 4 | 3.719 | 3.025 | 2.07 | 1.357 | 0.825 | 0.487 | 0.265 | 0.138 |
| Juni 2104 | 25 | 3 | 4 | 4 | 4 | 3.86 | 3.453 | 2.824 | 2.089 | 1.497 | 0.896 | 0.516 | 0.29 | 0.156 |
| Juni 2104 | 27 | 3 | 4 | 4 | 3.875 | 3.667 | 3.181 | 2.445 | 1.644 | 1.037 | 0.598 | 0.332 | 0.175 | 0.095 |
| Juni 2104 | 29 | 3 | 4 | 4 | 4 | 4 | 3.588 | 2.656 | 1.765 | 1.049 | 0.588 | 0.319 | 0.176 | 0.089 |
| Juni 2104 | 31 | 3 | 4 | 4 | 3.894 | 3.689 | 3.043 | 2.225 | 1.52 | 1.034 | 0.614 | 0.347 | 0.193 | 0.101 |

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| Test protein: SAR 0280-28-820 | | | | | | | | | | | | | | |
|-------------------------------|-------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID | No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| juni 280 | 60 | 3 | 4 | 4 | 4 | 3.777 | 3.441 | 2.735 | 1.958 | 1.293 | 0.733 | 0.428 | 0.246 | 0.12 |
| juni 280 | 61 | 3 | 4 | 4 | 4 | 4 | 3.789 | 3.282 | 2.436 | 1.6 | 0.979 | 0.547 | 0.262 | 0.121 |
| juni 280 | 62 | 3 | 3.894 | 3.892 | 3.897 | 3.871 | 3.544 | 3.122 | 2.573 | 2.006 | 1.383 | 0.841 | 0.481 | 0.252 |
| juni 280 | 63 | 3 | 4 | 4 | 4 | 4 | 3.719 | 3.025 | 2.07 | 1.357 | 0.825 | 0.487 | 0.265 | 0.138 |
| juni 280 | 64 | 3 | 4 | 4 | 4 | 3.86 | 3.453 | 2.824 | 2.089 | 1.497 | 0.896 | 0.516 | 0.29 | 0.156 |
| juni 280 | 65 | 3 | 4 | 4 | 3.875 | 3.667 | 3.181 | 2.445 | 1.644 | 1.037 | 0.598 | 0.332 | 0.175 | 0.095 |
| juni 280 | 66 | 3 | 4 | 4 | 4 | 4 | 3.588 | 2.656 | 1.765 | 1.049 | 0.588 | 0.319 | 0.176 | 0.089 |
| juni 280 | 67 | 3 | 4 | 4 | 3.894 | 3.689 | 3.043 | 2.225 | 1.52 | 1.034 | 0.614 | 0.347 | 0.193 | 0.101 |

| Test protein: SAR 0390-21-190 | | | | | | | | | | | | | | |
|-------------------------------|-------|---------|--------------------------|-------|-----|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID | No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| juni 0390* | 50 | 3 | 4 | 4 | 4 | 4 | 3.593 | 2.83 | 1.979 | 1.253 | 0.714 | 0.389 | 0.208 | 0.121 |
| juni 0390** | 51 | 3 | 4 | 4 | 4 | 3.925 | 3.627 | 2.731 | 1.785 | 1.053 | 0.574 | 0.296 | 0.155 | 0.081 |
| juni 0390 | 52 | 3 | 4 | 4 | 4 | 4 | 3.516 | 2.709 | 1.86 | 1.11 | 0.627 | 0.333 | 0.182 | 0.095 |
| juni 0390 | 53 | 3 | 4 | 4 | 4 | 4 | 3.753 | 3.297 | 2.379 | 1.538 | 0.917 | 0.502 | 0.278 | 0.15 |
| juni 0390 | 54 | 3 | 4 | 4 | 4 | 4 | 3.865 | 3.446 | 2.648 | 1.799 | 1.077 | 0.6 | 0.337 | 0.163 |
| juni 0390 | 55 | 3 | 4 | 4 | 4 | 4 | 3.931 | 3.907 | 3.544 | 2.769 | 1.844 | 1.107 | 0.612 | 0.316 |
| juni 0390 | 56 | 3 | 4 | 4 | 4 | 3.864 | 3.396 | 2.59 | 1.715 | 1.043 | 0.584 | 0.317 | 0.173 | 0.093 |
| juni 0390 | 57 | 3 | 4 | 3.931 | 4 | 3.841 | 3.233 | 2.309 | 1.443 | 0.83 | 0.45 | 0.234 | 0.123 | 0.067 |

| Test protein: SAR0222-27-609 | | | | | | | | | | | | | | |
|------------------------------|-------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 222 | 0Ø | 3 | 3.899 | 3.646 | 3.306 | 2.755 | 2.035 | 1.351 | 0.806 | 0.485 | 0.289 | 0.177 | 0.098 | 0.06 |
| 222 | BØ | 3 | 3.011 | 2.854 | 2.518 | 1.964 | 1.485 | 0.969 | 0.607 | 0.375 | 0.243 | 0.128 | 0.077 | 0.04 |
| 222 | VØ | 3 | 3.669 | 3.294 | 2.737 | 1.98 | 1.314 | 0.784 | 0.451 | 0.268 | 0.175 | 0.098 | 0.063 | 0.034 |
| 222 | HØ | 3 | 3.535 | 3.375 | 3.24 | 2.814 | 2.317 | 1.824 | 1.466 | 1.166 | 0.889 | 0.576 | 0.344 | 0.185 |
| 222 | 20Ø | 3 | 3.055 | 2.927 | 2.803 | 2.498 | 1.949 | 1.513 | 1.087 | 0.756 | 0.481 | 0.283 | 0.157 | 0.086 |

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| Test protein: SAR0222-27-609 | | | | | | | | | | | | | |
|------------------------------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 222 2BØ | 3 | 2,568 | 2.281 | 1.871 | 1.331 | 0.84 | 0.471 | 0.267 | 0.145 | 0.084 | 0.049 | 0.029 | 0.017 |
| 222 2HØ | 3 | 4 | 3.816 | 3.646 | 3.093 | 2.389 | 1.66 | 1.033 | 0.628 | 0.415 | 0.25 | 0.143 | 0.077 |
| 222 2VØ | 3 | 4 | 3.827 | 3.552 | 3.05 | 2.385 | 1.665 | 1.065 | 0.642 | 0.365 | 0.203 | 0.127 | 0.062 |

| Test protein: SAR0872-27-273 | | | | | | | | | | | | | |
|------------------------------|---------|--------------------------|-----|-----|-----|------|------|------|-------|-------|-------|--------|--------|
| ELISA Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 0872 2 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.564 | 2.528 | 1.57 |
| 0872 4 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.944 | 3.476 | 2.441 | 1.561 | 0.917 |
| 0872 6 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.931 | 3.367 | 2.446 | 1.57 |
| 0872 8 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.777 | 2.732 | 1.739 |
| 0872 17 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.724 | 2.838 | 1.913 | 1.158 |
| 0872 19 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.786 | 3.121 | 2.237 | 1.409 | 0.811 |
| 0872 21 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.566 | 2.552 | 1.615 | 0.901 |
| 0872 23 | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.887 | 3.269 | 2.251 | 1.404 |

| Test protein: SAR1879-24-184 | | | | | | | | | | | | | |
|------------------------------|---------|--------------------------|-----|-----|-----|------|-------|-------|-------|-------|-------|--------|--------|
| ELISA Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 1879 0Ø | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.871 | 3.028 | 2.038 | 1.228 | 0.662 |
| 1879 VØ | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 3.508 | 2.428 | 1.548 | 0.881 | 0.478 | 0.242 |
| 1879 HØ | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 3.665 | 2.686 | 1.778 | 1.041 | 0.577 | 0.301 |
| 1879 20Ø | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 3.501 | 2.468 | 1.548 | 0.856 | 0.474 | 0.244 |
| 1879 2BØ | 3 | 4 | 4 | 4 | 4 | 4 | 3.872 | 3.175 | 2.12 | 1.333 | 0.747 | 0.406 | 0.213 |
| 1879 2VØ | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 3.52 | 2.453 | 1.483 | 0.821 | 0.428 |
| 1879 2HØ | 3 | 4 | 4 | 4 | 4 | 4 | 3.885 | 3.363 | 2.325 | 1.452 | 0.826 | 0.448 | 0.224 |

| Test protein: SAR1881-25-208 | | | | | | | | | | | | | |
|------------------------------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 1881 0Ø | 3 | 4 | 4 | 3.66 | 3.06 | 2.238 | 1.454 | 0.848 | 0.47 | 0.251 | 0.135 | 0.078 | 0.047 |
| 1881 BØ | 3 | 4 | 4 | 3.558 | 2.546 | 1.551 | 0.884 | 0.481 | 0.26 | 0.137 | 0.075 | 0.048 | 0.032 |
| 1881 VØ | 3 | 4 | 4 | 3.78 | 2.952 | 1.888 | 1.105 | 0.617 | 0.335 | 0.181 | 0.102 | 0.058 | 0.039 |
| 1881 HØ | 3 | 4 | 3.595 | 2.644 | 1.678 | 0.983 | 0.546 | 0.3 | 0.162 | 0.091 | 0.053 | 0.035 | 0.026 |
| 1881 20Ø | 3 | 4 | 4 | 4 | 4 | 3.583 | 3.018 | 2.231 | 1.454 | 0.866 | 0.478 | 0.258 | 0.141 |
| 1881 2BØ | 3 | 1.195 | 0.577 | 0.316 | 0.171 | 0.101 | 0.064 | 0.044 | 0.032 | 0.027 | 0.022 | 0.022 | 0.019 |
| 1881 2VØ | 3 | 4 | 3.792 | 3.313 | 2.508 | 1.716 | 1.024 | 0.598 | 0.333 | 0.181 | 0.1 | 0.06 | 0.039 |
| 1881 2HØ | 3 | 0.995 | 0.559 | 0.3 | 0.165 | 0.097 | 0.061 | 0.043 | 0.033 | 0.026 | 0.02 | 0.019 | 0.02 |

| Test protein: SAR2104-20-154 | | | | | | | | | | | | | |
|------------------------------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 2104 0Ø | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 3.841 | 3.033 | 2.031 | 1.197 | 0.674 | 0.371 |
| 2104 BØ | 3 | 0.67 | 0.377 | 0.22 | 0.138 | 0.089 | 0.067 | 0.052 | 0.048 | 0.044 | 0.042 | 0.041 | 0.04 |
| 2104 VØ | 3 | 0.276 | 0.165 | 0.099 | 0.073 | 0.057 | 0.053 | 0.047 | 0.045 | 0.043 | 0.042 | 0.041 | 0.039 |

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| Test protein: SAR2104-20-154 | | | | | | | | | | | | | | |
|------------------------------|-------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 2104 | 2OØ | 3 | 0.153 | 0.099 | 0.071 | 0.057 | 0.048 | 0.047 | 0.043 | 0.043 | 0.044 | 0.042 | 0.041 | 0.039 |
| 2104 | 2BØ | 3 | 0.458 | 0.378 | 0.285 | 0.244 | 0.2 | 0.169 | 0.135 | 0.099 | 0.07 | 0.052 | 0.047 | 0.043 |
| 2104 | 2VØ | 3 | 0.349 | 0.25 | 0.178 | 0.133 | 0.098 | 0.09 | 0.067 | 0.041 | 0.046 | 0.043 | 0.042 | 0.039 |
| 2104 | 2HØ | 3 | 0.345 | 0.221 | 0.142 | 0.103 | 0.074 | 0.06 | 0.051 | 0.047 | 0.044 | 0.041 | 0.042 | 0.037 |

| Test protein: SAR2119-34-370 | | | | | | | | | | | | | | |
|------------------------------|-------|---------|--------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 2119 | OØ | 3 | 4 | 4 | 4 | 3.857 | 4 | 4 | 3.689 | 3.27 | 1.839 | 1.121 | 0.597 | 0.311 |
| 2119 | BØ | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 3.872 | 3.379 | 2.373 | 1.49 | 0.827 | 0.434 |
| 2119 | VØ | 3 | 4 | 4 | 3.949 | 4 | 4 | 4 | 3.892 | 3.218 | 2.22 | 1.339 | 0.751 | 0.381 |
| 2119 | HØ | 3 | 0.187 | 0.101 | 0.168 | 0.102 | 0.062 | 0.041 | 0.03 | 0.022 | 0.017 | 0.017 | 0.015 | 0.011 |
| 2119 | 2OØ | 3 | 4 | 4 | 4 | 4 | 3.421 | 2.446 | 1.457 | 0.819 | 0.439 | 0.228 | 0.122 | 0.063 |
| 2119 | 2BØ | 3 | 4 | 4 | 4 | 4 | 4 | 4 | 3.594 | 2.695 | 1.747 | 1.026 | 0.547 | |
| 2119 | 2VØ | 3 | 4 | 4 | 4 | 4 | 3.577 | 2.731 | 1.734 | 1.012 | 0.552 | 0.285 | 0.146 | 0.076 |
| 2119 | 2HØ | 3 | 4 | 4 | 4 | 4 | 3.498 | 2.52 | 1.521 | 0.874 | 0.466 | 0.244 | 0.128 | 0.066 |

| Test protein: SAR2718-24-157 | | | | | | | | | | | | | | |
|------------------------------|-------|---------|--------------------------|-----|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID No | | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 2718 | OØ | 3 | 4 | 4 | 4 | 4 | 4 | 3.906 | 3.27 | 2.491 | 1.673 | 1.062 | 0.616 | 0.323 |
| 2718 | VØ | 3 | 3.923 | 4 | 4 | 3.786 | 3.09 | 2.101 | 1.238 | 0.682 | 0.366 | 0.19 | 0.105 | 0.057 |
| 2718 | HØ | 3 | 4 | 4 | 4 | 4 | 4 | 3.944 | 3.498 | 2.547 | 1.622 | 0.963 | 0.514 | 0.27 |
| 2718 | 2OØ | 3 | 4 | 4 | 4 | 4 | 4 | 3.944 | 2.971 | 1.885 | 0.966 | 0.449 | 0.187 | 0.086 |
| 2718 | 2BØ | 3 | 4 | 4 | 3.885 | 3.344 | 3.204 | 1.371 | 0.773 | 0.402 | 0.216 | 0.115 | 0.06 | 0.037 |
| 2718 | 2VØ | 3 | 4 | 4 | 4 | 4 | 3.801 | 2.893 | 1.911 | 1.17 | 0.632 | 0.349 | 0.174 | 0.091 |
| 2718 | 2HØ | 3 | 4 | 4 | 4 | 3.726 | 3.229 | 1.844 | 1.104 | 0.595 | 0.324 | 0.174 | 0.093 | 0.051 |

| Test protein: SAR0826-42-209 | | | | | | | | | | | | | | |
|------------------------------|-------|---------|--------------------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| ELISA | Mouse | Bleed | Sera dilution (OD490 nm) | | | | | | | | | | | |
| Plate ID | No | Bleed # | 100 | 200 | 400 | 800 | 1600 | 3200 | 6400 | 12800 | 25600 | 51200 | 102400 | 204800 |
| 0826 | 1 | 3 | -0.0058 | -0.0288 | -0.0138 | -0.0258 | -0.0128 | -0.0288 | 0.0132 | 0.0062 | -0.0688 | -0.0098 | -0.0398 | -0.0178 |
| 0826 | 2 | 3 | 0.2672 | -0.0188 | -0.0668 | -0.0888 | -0.1188 | -0.1038 | -0.1288 | -0.1168 | -0.1188 | -0.1068 | -0.0698 | 0.3492 |
| 0826 | 3 | 3 | -0.0828 | -0.1518 | -0.1278 | -0.1308 | -0.1268 | -0.1168 | -0.1288 | -0.1338 | -0.0558 | -0.1118 | -0.0968 | -0.0378 |
| 0826 | 4 | 3 | -0.0918 | -0.1458 | -0.1308 | -0.1448 | -0.1408 | -0.1318 | -0.1518 | -0.1398 | -0.1328 | -0.1168 | -0.1068 | -0.0588 |
| 0826 | 5 | 3 | 0.0922 | -0.1228 | -0.1448 | -0.1438 | -0.1168 | -0.1198 | -0.0918 | -0.1388 | -0.1288 | -0.1138 | -0.1228 | -0.0908 |
| 0826 | 6 | 3 | 1.1902 | 0.4132 | 0.0792 | -0.0518 | -0.1048 | -0.1448 | -0.1378 | -0.1568 | -0.1378 | -0.1168 | -0.1168 | -0.0678 |
| 0826 | 7 | 3 | 3.1572 | 2.6172 | 1.6322 | 0.8702 | 0.3652 | 0.1352 | -0.0218 | -0.0928 | -0.0928 | -0.0928 | -0.0988 | -0.0948 |
| 0826 | 8 | 3 | -0.1568 | -0.1638 | -0.1168 | -0.1198 | -0.0238 | 0.0102 | -0.0388 | -0.0828 | -0.0818 | -0.0618 | -0.0368 | -0.0038 |

Immune Fluorescence/FACS Analyses of Plasma Samples from Immunized Mice

1. Groups of mice will be immunized three times with intervals of 14 days with antigen coupled onto carrier-proteins, diphtheria-toxoid and/or secreted mycobacterial proteins (PPD). All immunizations are carried out subcuta-

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neously with the antigen adsorbed onto Al(OH)₃ and with Freund's incomplete adjuvant, cf. above.

2. A control group of mice are immunized with diphtheria-toxoid without antigen.

65

3. Mice are bled after the second and the third immunization.

- 4. The serum bleeds are tested for their reactivity against the immunizing antigen.
- 5. The following methods will be used:
 Direct measurement of antibodies to the immunizing antigen
 Analysis for agglutinating power when antibodies are incubated with the bacteria

Analysis for killing effect on bacteria after incubation of bacteria with antiserum+fresh serum (complement)
 Proteins of the Invention
 The *S. aureus* proteins of the present invention are set forth in the sequence listing together with their related nucleic acid sequences. For easy reference, the one letter amino acid sequences of the *S. aureus* proteins are provided in the following:

SEQ ID NO: 1:
 MKRLLGLLLVSTLVLSACGNDENQEESKKEVKSKEKKI EKEKENKSKDKKEKVA TQQQPDNQTV EQPQ
 SQEQSVQQPQQQIPQNSVPPQNVQVQQNKQKVDLNNMPPPTDFSTEGMSEQAQKQIEELSMQKDYHG
 LSQREYNDRVSEIINNDN

SEQ ID NO: 2:
 MLKGCGLISPIIILII LLSACSMFNSNDNSTSNQSSKTQLTQKDEDKSENMPEEKSESETDKDLQSTE
 EVPANENTENNQHEIDEITTTDQSDDEINTPNVAEEESQDDLKDDLKEKQPSDHHQSTQPKTSPSTETN
 KQQSFANCKQLRQVYPNGVTADHPAYRPHLDRDKKRA CEPDKY

SEQ ID NO: 3:
 MKKLIISIMAIMLFLTGCCKS QEKATLEKDI DNQKENKELDKKEKQEQEKEKLADKQKDL EKEVKDLKP
 SKEDNKDDKDEDKNKDKKEASQDKQSKDQTKS SDKDNHKKPTSTDKDQKANDKHQS

SEQ ID NO: 4:
 MKNAPKLPKMDLKKVAKT PAVWII LAGLAILPSFYAWFNLWAMWDPYGN TGHIKVAVVNEDKGD TIRGK
 KVNVGNTMVNTLKKNKSPDWQFVSREKADHEIKMGKYFAGIYIPSKFTHEITGTLRKPQKADVEFKV NQ
 KINAVASKLTDTGSSVVVEKANEQFNKTVTRALLEEANKAGLTI EENVPTINKIKNAVYSADKALPKINDFA
 NKIVYLNNHQADLDKYANDFRKLGNYKGDILDAQKLLNEVNGAIPQLNEKAKLILALNNYMPKIEKALNFA
 ADDVPAQFPKINQGLNIASQGDIDQANGQLNDAKGFVTQVRSRVGDYQEAIRRAQDLNRRNQQQIPQNS
 AANNETSNSAPAAGNGVTSTPPSAPNGNTIPNNVNTQNTAPNSNNA PVSTTPQSTSGKKDGGQSFADITT
 TQVSTANENTQNIITDKDVKSMEEALTGSLLSLNNLDTQAKAAQKDSQALRNI SYGILASDKPSDFRESL
 DNVKSGLEYTTQYNQQFIDTLKEIEKNENVDL SKEIDKVKTANNRINESLRLVNQLSNALKNNGSSTAEAT
 KLLDQLSKLSSLSFRDYVKKDLNSSLVSI SQRIMDELNKGQTALSNVQSKLNTIDQVINSGQ SILKNG
 KTRIDRLQTVLPSIEQQYISAIKNAQANFPKVKSDVAKAANFVRNDLPQLEQRLTNATASVKNLPTLLNG
 YDQAVGLLNKNQPAKALSDLADFQNKLPDVEKDLK KANKIFKKLDKDDAVDKLIDTLKNDLKKQAGI
 IANPINKKTVDVFPVKDYSGMTPFYTALSVWVGALLMVSLLTVDNKHKSLEPVLTTTRQVFLGKAGFFIML
 GMLQALIVSVGDLILLKAGVESFVLFVLI TIFCSIIFNSIVYTCVSL LGNPGKAI AIVLLVLQIAGGGGTFPIQT
 TPQFFQNISPYLPFTYAIDSLRETVGGIVPEILITKLI I LTLFGIGFFVVG LILKPVTDPLMKRVSEKVDQSNVT
 E

SEQ ID NO: 5:
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SEQUENCE LISTING

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 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 1

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 50 55 60
 Val Glu Gln Pro Gln Ser Gln Glu Gln Ser Val Gln Gln Pro Gln Gln
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 85 90 95
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| Asn | Asn | Glu | Thr | Ser | Asn | Ser | Ala | Pro | Ala | Ala | Gly | Asn | Gly | Val | Thr |
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| Ser | Thr | Pro | Pro | Ser | Ala | Pro | Asn | Gly | Asn | Thr | Thr | Pro | Asn | Asn | Asn |
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| Thr | Pro | Gln | Ser | Thr | Ser | Gly | Lys | Lys | Asp | Gly | Gln | Ser | Phe | Ala | Asp |
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| Thr | Asp | Lys | Asp | Val | Lys | Ser | Met | Glu | Ala | Ala | Leu | Thr | Gly | Ser | Leu |
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| Leu | Ser | Leu | Ser | Asn | Asn | Leu | Asp | Thr | Gln | Ala | Lys | Ala | Ala | Gln | Lys |
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Pro Val Leu Phe Val Leu Ile Thr Ile Phe Cys Ser Ile Ile Phe Asn
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885 890 895

Ile Ala Ile Val Leu Leu Val Leu Gln Ile Ala Gly Gly Gly Gly Thr
900 905 910

Phe Pro Ile Gln Thr Thr Pro Gln Phe Phe Gln Asn Ile Ser Pro Tyr
915 920 925

Leu Pro Phe Thr Tyr Ala Ile Asp Ser Leu Arg Glu Thr Val Gly Gly
930 935 940

Ile Val Pro Glu Ile Leu Ile Thr Lys Leu Ile Ile Leu Thr Leu Phe
945 950 955 960

Gly Ile Gly Phe Phe Val Val Gly Leu Ile Leu Lys Pro Val Thr Asp
965 970 975

Pro Leu Met Lys Arg Val Ser Glu Lys Val Asp Gln Ser Asn Val Thr
980 985 990

Glu

<210> SEQ ID NO 5
<211> LENGTH: 2066
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 5

Met Asn Glu Lys Val Glu Gly Met Thr Leu Glu Leu Lys Leu Asp His
1 5 10 15

Leu Gly Val Gln Glu Gly Met Lys Gly Leu Lys Arg Gln Leu Gly Val
20 25 30

Val Asn Ser Glu Met Lys Ala Asn Leu Ser Ala Phe Asp Lys Ser Glu
35 40 45

Lys Ser Met Glu Lys Tyr Gln Ala Arg Ile Lys Gly Leu Asn Asp Arg
50 55 60

Leu Lys Val Gln Lys Lys Met Tyr Ser Gln Val Glu Asp Glu Leu Lys
65 70 75 80

Gln Val Asn Ala Asn Tyr Gln Lys Ala Lys Ser Ser Val Lys Asp Val
85 90 95

Glu Lys Ala Tyr Leu Lys Leu Val Glu Ala Asn Lys Lys Glu Lys Leu
100 105 110

Ala Leu Asp Lys Ser Lys Glu Ala Leu Lys Ser Ser Asn Thr Glu Leu
115 120 125

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Lys Lys Ala Glu Asn Gln Tyr Lys Arg Thr Asn Gln Arg Lys Gln Asp
 130 135 140
 Ala Tyr Gln Lys Leu Lys Gln Leu Arg Asp Ala Glu Gln Lys Leu Lys
 145 150 155 160
 Asn Ser Asn Gln Ala Thr Thr Ala Gln Leu Lys Arg Ala Ser Asp Ala
 165 170 175
 Val Gln Lys Gln Ser Ala Lys His Lys Ala Leu Val Glu Gln Tyr Lys
 180 185 190
 Gln Glu Gly Asn Gln Val Gln Lys Leu Lys Val Gln Asn Asp Asn Leu
 195 200 205
 Ser Lys Ser Asn Asp Lys Ile Glu Ser Ser Tyr Ala Lys Thr Asn Thr
 210 215 220
 Lys Leu Lys Gln Thr Glu Lys Glu Phe Asn Asp Leu Asn Asn Thr Ile
 225 230 235 240
 Lys Asn His Ser Ala Asn Val Ala Lys Ala Glu Thr Ala Val Asn Lys
 245 250 255
 Glu Lys Ala Ala Leu Asn Asn Leu Glu Arg Ser Ile Asp Lys Ala Ser
 260 265 270
 Ser Glu Met Lys Thr Phe Asn Lys Glu Gln Met Ile Ala Gln Ser His
 275 280 285
 Phe Gly Lys Leu Ala Ser Gln Ala Asp Val Met Ser Lys Lys Phe Ser
 290 295 300
 Ser Ile Gly Asp Lys Met Thr Ser Leu Gly Arg Thr Met Thr Met Gly
 305 310 315 320
 Val Ser Thr Pro Ile Thr Leu Gly Leu Gly Ala Ala Leu Lys Thr Ser
 325 330 335
 Ala Asp Phe Glu Gly Gln Met Ser Arg Val Gly Ala Ile Ala Gln Ala
 340 345 350
 Ser Ser Lys Asp Leu Lys Ser Met Ser Asn Gln Ala Val Asp Leu Gly
 355 360 365
 Ala Lys Thr Ser Lys Ser Ala Asn Glu Val Ala Lys Gly Met Glu Glu
 370 375 380
 Leu Ala Ala Leu Gly Phe Asn Ala Lys Gln Thr Met Glu Ala Met Pro
 385 390 395 400
 Gly Val Ile Ser Ala Ala Glu Ala Ser Gly Ala Glu Met Ala Thr Thr
 405 410 415
 Ala Thr Val Met Ala Ser Ala Ile Asn Ser Phe Gly Leu Lys Ala Ser
 420 425 430
 Asp Ala Asn His Val Ala Asp Leu Leu Ala Arg Ser Ala Asn Asp Ser
 435 440 445
 Ala Ala Asp Ile Gln Tyr Met Gly Asp Ala Leu Lys Tyr Ala Gly Thr
 450 455 460
 Pro Ala Lys Ala Leu Gly Val Ser Ile Glu Asp Thr Ser Ala Ala Ile
 465 470 475 480
 Glu Val Leu Ser Asn Ser Gly Leu Glu Gly Ser Gln Ala Gly Thr Ala
 485 490 495
 Leu Arg Ala Ser Phe Ile Arg Leu Ala Asn Pro Ser Lys Asn Thr Ala
 500 505 510
 Lys Glu Met Lys Lys Leu Gly Ile His Leu Ser Asp Ala Lys Gly Gln
 515 520 525
 Phe Val Gly Met Gly Glu Leu Ile Arg Gln Phe Gln Asp Asn Met Lys
 530 535 540

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Gly Met Thr Arg Glu Gln Lys Leu Ala Thr Val Ala Thr Ile Val Gly
 545 550 555 560
 Thr Glu Ala Ala Ser Gly Phe Leu Ala Leu Ile Glu Ala Gly Pro Asp
 565 570 575
 Lys Ile Asn Ser Tyr Ser Lys Ser Leu Lys Asn Ser Asn Gly Glu Ser
 580 585 590
 Lys Lys Ala Ala Asp Leu Met Lys Asp Asn Leu Lys Gly Ala Leu Glu
 595 600 605
 Gln Leu Gly Gly Ala Phe Glu Ser Leu Ala Ile Glu Val Gly Lys Asp
 610 615 620
 Leu Thr Pro Met Ile Arg Ala Gly Ala Glu Gly Leu Thr Lys Leu Val
 625 630 635 640
 Asp Gly Phe Thr His Leu Pro Gly Trp Val Arg Lys Ala Ser Val Gly
 645 650 655
 Leu Ala Leu Phe Gly Ala Ser Ile Gly Pro Ala Val Leu Ala Gly Gly
 660 665 670
 Leu Leu Ile Arg Ala Val Gly Ser Ala Ala Lys Gly Tyr Ala Ser Leu
 675 680 685
 Asn Arg Arg Ile Ala Glu Asn Thr Ile Leu Ser Asn Thr Asn Ser Lys
 690 695 700
 Ala Met Lys Ser Leu Gly Leu Gln Thr Leu Phe Leu Gly Ser Thr Thr
 705 710 715 720
 Gly Lys Thr Ser Lys Gly Phe Lys Gly Leu Ala Gly Ala Met Leu Phe
 725 730 735
 Asn Leu Lys Pro Ile Asn Val Leu Lys Asn Ser Ala Lys Leu Ala Ile
 740 745 750
 Leu Pro Phe Lys Leu Leu Lys Asn Gly Leu Gly Leu Ala Ala Lys Ser
 755 760 765
 Leu Phe Ala Val Ser Gly Gly Ala Arg Phe Ala Gly Val Ala Leu Lys
 770 775 780
 Phe Leu Thr Gly Pro Ile Gly Ala Thr Ile Thr Ala Ile Thr Ile Ala
 785 790 795 800
 Tyr Lys Val Phe Lys Thr Ala Tyr Asp Arg Val Glu Trp Phe Arg Asn
 805 810 815
 Gly Ile Asn Gly Leu Gly Glu Thr Ile Lys Phe Phe Gly Gly Lys Ile
 820 825 830
 Ile Gly Gly Ala Val Arg Lys Leu Gly Glu Phe Lys Asn Tyr Leu Gly
 835 840 845
 Ser Ile Gly Lys Ser Phe Lys Glu Lys Phe Ser Lys Asp Met Lys Asp
 850 855 860
 Gly Tyr Lys Ser Leu Ser Asp Asp Leu Leu Lys Val Gly Val Asn
 865 870 875 880
 Lys Phe Lys Gly Phe Met Gln Thr Met Gly Thr Ala Ser Lys Lys Ala
 885 890 895
 Ser Asp Thr Val Lys Val Leu Gly Lys Gly Val Ser Lys Glu Thr Glu
 900 905 910
 Lys Ala Leu Glu Lys Tyr Val His Tyr Ser Glu Glu Asn Asn Arg Ile
 915 920 925
 Met Glu Lys Val Arg Leu Asn Ser Gly Gln Ile Thr Glu Asp Lys Ala
 930 935 940
 Lys Lys Leu Leu Lys Ile Glu Ala Asp Leu Ser Asn Asn Leu Ile Ala
 945 950 955 960
 Glu Ile Glu Lys Arg Asn Lys Lys Glu Leu Glu Lys Thr Gln Glu Leu

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| 965 | | | | | 970 | | | | | 975 | | | | | |
|-----|------|-----|-----|-----|-----|------|------|-----|-----|-----|------|-----|------|-----|-----|
| Ile | Asp | Lys | Tyr | Ser | Ala | Phe | Asp | Glu | Gln | Glu | Lys | Gln | Asn | Ile | Leu |
| | | | 980 | | | | | 985 | | | | | 990 | | |
| Thr | Arg | Thr | Lys | Glu | Lys | Asn | Asp | Leu | Arg | Ile | Lys | Lys | Glu | Gln | Glu |
| | | 995 | | | | | 1000 | | | | | | 1005 | | |
| Leu | Asn | Gln | Lys | Ile | Lys | Glu | Leu | Lys | Glu | Lys | Ala | Leu | Ser | Asp | |
| | 1010 | | | | | 1015 | | | | | 1020 | | | | |
| Gly | Gln | Ile | Ser | Glu | Asn | Glu | Arg | Lys | Glu | Ile | Glu | Lys | Leu | Glu | |
| | 1025 | | | | | 1030 | | | | | 1035 | | | | |
| Asn | Gln | Arg | Arg | Asp | Ile | Thr | Val | Lys | Glu | Leu | Ser | Lys | Thr | Glu | |
| | 1040 | | | | | 1045 | | | | | 1050 | | | | |
| Lys | Glu | Gln | Glu | Arg | Ile | Leu | Val | Arg | Met | Gln | Arg | Asn | Arg | Asn | |
| | 1055 | | | | | 1060 | | | | | 1065 | | | | |
| Ser | Tyr | Ser | Ile | Asp | Glu | Ala | Ser | Lys | Ala | Ile | Lys | Glu | Ala | Glu | |
| | 1070 | | | | | 1075 | | | | | 1080 | | | | |
| Lys | Ala | Arg | Lys | Ala | Lys | Lys | Lys | Glu | Val | Asp | Lys | Gln | Tyr | Glu | |
| | 1085 | | | | | 1090 | | | | | 1095 | | | | |
| Asp | Asp | Val | Ile | Ala | Ile | Lys | Asn | Asn | Val | Asn | Leu | Ser | Lys | Ser | |
| | 1100 | | | | | 1105 | | | | | 1110 | | | | |
| Glu | Lys | Asp | Lys | Leu | Leu | Ala | Ile | Ala | Asp | Gln | Arg | His | Lys | Asp | |
| | 1115 | | | | | 1120 | | | | | 1125 | | | | |
| Glu | Val | Arg | Lys | Ala | Lys | Ser | Lys | Lys | Asp | Ala | Val | Val | Asp | Val | |
| | 1130 | | | | | 1135 | | | | | 1140 | | | | |
| Val | Lys | Lys | Gln | Asn | Lys | Asp | Ile | Asp | Lys | Glu | Met | Asp | Leu | Ser | |
| | 1145 | | | | | 1150 | | | | | 1155 | | | | |
| Ser | Gly | Arg | Val | Tyr | Lys | Asn | Thr | Glu | Lys | Trp | Trp | Asn | Gly | Leu | |
| | 1160 | | | | | 1165 | | | | | 1170 | | | | |
| Lys | Ser | Trp | Trp | Ser | Asn | Phe | Arg | Glu | Asp | Gln | Lys | Lys | Lys | Ser | |
| | 1175 | | | | | 1180 | | | | | 1185 | | | | |
| Asp | Lys | Tyr | Ala | Lys | Glu | Gln | Glu | Glu | Thr | Ala | Arg | Arg | Asn | Arg | |
| | 1190 | | | | | 1195 | | | | | 1200 | | | | |
| Glu | Asn | Ile | Lys | Lys | Trp | Phe | Gly | Asn | Ala | Trp | Asp | Gly | Val | Lys | |
| | 1205 | | | | | 1210 | | | | | 1215 | | | | |
| Ser | Lys | Thr | Gly | Glu | Ala | Phe | Ser | Lys | Met | Gly | Arg | Asn | Ala | Asn | |
| | 1220 | | | | | 1225 | | | | | 1230 | | | | |
| His | Phe | Gly | Gly | Glu | Met | Lys | Lys | Met | Trp | Ser | Gly | Ile | Lys | Gly | |
| | 1235 | | | | | 1240 | | | | | 1245 | | | | |
| Ile | Pro | Ser | Lys | Leu | Ser | Ser | Gly | Trp | Ser | Ser | Ala | Lys | Ser | Ser | |
| | 1250 | | | | | 1255 | | | | | 1260 | | | | |
| Val | Gly | Tyr | His | Thr | Lys | Ala | Ile | Ala | Asn | Ser | Thr | Gly | Lys | Trp | |
| | 1265 | | | | | 1270 | | | | | 1275 | | | | |
| Phe | Gly | Lys | Ala | Trp | Gln | Ser | Val | Lys | Ser | Thr | Thr | Gly | Ser | Ile | |
| | 1280 | | | | | 1285 | | | | | 1290 | | | | |
| Tyr | Asn | Gln | Thr | Lys | Gln | Lys | Tyr | Ser | Asp | Ala | Ser | Asp | Lys | Ala | |
| | 1295 | | | | | 1300 | | | | | 1305 | | | | |
| Trp | Ala | His | Ser | Lys | Ser | Ile | Trp | Lys | Gly | Thr | Ser | Lys | Trp | Phe | |
| | 1310 | | | | | 1315 | | | | | 1320 | | | | |
| Ser | Asn | Ala | Tyr | Lys | Ser | Ala | Lys | Gly | Trp | Leu | Thr | Asp | Met | Ala | |
| | 1325 | | | | | 1330 | | | | | 1335 | | | | |
| Asn | Lys | Ser | Arg | Ser | Lys | Trp | Asp | Asn | Ile | Ser | Ser | Thr | Ala | Trp | |
| | 1340 | | | | | 1345 | | | | | 1350 | | | | |
| Ser | Asn | Ala | Lys | Ser | Val | Trp | Lys | Gly | Thr | Ser | Lys | Trp | Phe | Ser | |
| | 1355 | | | | | 1360 | | | | | 1365 | | | | |

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| |
|---|
| Asn Ser Tyr Lys Ser Leu Lys Gly Trp Thr Gly Asp Met Tyr Ser 1370 1375 1380 |
| Arg Ala His Asp Arg Phe Asp Ala Ile Ser Ser Ser Ala Trp Ser 1385 1390 1395 |
| Asn Ala Lys Ser Val Phe Asn Gly Phe Arg Lys Trp Leu Ser Arg 1400 1405 1410 |
| Thr Tyr Glu Trp Ile Arg Asp Ile Gly Lys Asp Met Gly Arg Ala 1415 1420 1425 |
| Ala Ala Asp Leu Gly Lys Asn Val Ala Asn Lys Ala Ile Gly Gly 1430 1435 1440 |
| Leu Asn Ser Met Ile Gly Gly Ile Asn Lys Ile Ser Lys Ala Ile 1445 1450 1455 |
| Thr Asp Lys Asn Leu Ile Lys Pro Ile Pro Thr Leu Ser Thr Gly 1460 1465 1470 |
| Thr Leu Ala Gly Lys Gly Val Ala Thr Asp Asn Ser Gly Ala Leu 1475 1480 1485 |
| Thr Gln Pro Thr Phe Ala Val Leu Asn Asp Arg Gly Ser Gly Asn 1490 1495 1500 |
| Ala Pro Gly Gly Gly Val Gln Glu Val Ile His Arg Ala Asp Gly 1505 1510 1515 |
| Thr Phe His Ala Pro Gln Gly Arg Asp Val Val Val Pro Leu Gly 1520 1525 1530 |
| Val Gly Asp Ser Val Ile Asn Ala Asn Asp Thr Leu Lys Leu Gln 1535 1540 1545 |
| Arg Met Gly Val Leu Pro Lys Phe His Gly Gly Thr Lys Lys Lys 1550 1555 1560 |
| Lys Trp Met Glu Gln Val Thr Glu Asn Leu Gly Lys Lys Ala Gly 1565 1570 1575 |
| Asp Phe Gly Ser Lys Ala Lys Asn Thr Ala His Asn Ile Lys Lys 1580 1585 1590 |
| Gly Ala Glu Glu Met Val Glu Ala Ala Gly Asp Lys Ile Lys Asp 1595 1600 1605 |
| Gly Ala Ser Trp Leu Gly Asp Lys Ile Gly Asp Val Trp Asp Tyr 1610 1615 1620 |
| Val Gln His Pro Gly Lys Leu Val Asn Lys Val Met Ser Gly Leu 1625 1630 1635 |
| Asn Ile Asn Phe Gly Gly Gly Ala Asn Ala Thr Val Lys Ile Ala 1640 1645 1650 |
| Lys Gly Ala Tyr Ser Leu Leu Lys Lys Lys Leu Val Asp Lys Val 1655 1660 1665 |
| Lys Ser Trp Phe Glu Asp Phe Gly Gly Gly Gly Asp Gly Ser Tyr 1670 1675 1680 |
| Leu Phe Asp His Pro Ile Trp Gln Arg Phe Gly Ser Tyr Thr Gly 1685 1690 1695 |
| Gly Leu Asn Phe Asn Gly Gly Arg His Tyr Gly Ile Asp Phe Gln 1700 1705 1710 |
| Met Pro Thr Gly Thr Asn Ile Tyr Ala Val Lys Gly Gly Ile Ala 1715 1720 1725 |
| Asp Lys Val Trp Thr Asp Tyr Gly Gly Gly Asn Ser Ile Gln Ile 1730 1735 1740 |
| Lys Thr Gly Ala Asn Glu Trp Asn Trp Tyr Met His Leu Ser Lys 1745 1750 1755 |

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Gln Leu Ala Arg Gln Gly Gln Arg Ile Lys Ala Gly Gln Leu Ile
 1760 1765 1770

Gly Lys Ser Gly Ala Thr Gly Asn Phe Val Arg Gly Ala His Leu
 1775 1780 1785

His Phe Gln Leu Met Gln Gly Ser His Pro Gly Asn Asp Thr Ala
 1790 1795 1800

Lys Asp Pro Glu Lys Trp Leu Lys Ser Leu Lys Gly Ser Gly Val
 1805 1810 1815

Arg Ser Gly Ser Gly Val Asn Lys Ala Ala Ser Ala Trp Ala Gly
 1820 1825 1830

Asp Ile Arg Arg Ala Ala Lys Arg Met Gly Val Asn Val Thr Ser
 1835 1840 1845

Gly Asp Val Gly Asn Ile Ile Ser Leu Ile Gln His Glu Ser Gly
 1850 1855 1860

Gly Asn Ala Gly Ile Thr Gln Ser Ser Ala Leu Arg Asp Ile Asn
 1865 1870 1875

Val Leu Gln Gly Asn Pro Ala Lys Gly Leu Leu Gln Tyr Ile Pro
 1880 1885 1890

Gln Thr Phe Arg His Tyr Ala Val Arg Gly His Asn Asn Ile Tyr
 1895 1900 1905

Ser Gly Tyr Asp Gln Leu Leu Ala Phe Phe Asn Asn Ser Tyr Trp
 1910 1915 1920

Arg Ser Gln Phe Asn Pro Arg Gly Gly Trp Ser Pro Ser Gly Pro
 1925 1930 1935

Arg Arg Tyr Ala Asn Gly Gly Leu Ile Thr Lys His Gln Leu Ala
 1940 1945 1950

Glu Val Gly Glu Gly Asp Lys Gln Glu Met Val Ile Pro Leu Thr
 1955 1960 1965

Arg Arg Lys Arg Ala Ile Gln Leu Thr Glu Gln Val Met Arg Ile
 1970 1975 1980

Ile Gly Met Asp Gly Lys Pro Asn Asn Ile Thr Val Asn Asn Asp
 1985 1990 1995

Thr Ser Thr Val Glu Lys Leu Leu Lys Gln Ile Val Met Leu Ser
 2000 2005 2010

Asp Lys Gly Asn Lys Leu Thr Asp Ala Leu Ile Gln Thr Val Ser
 2015 2020 2025

Ser Gln Asp Asn Asn Leu Gly Ser Asn Asp Ala Ile Arg Gly Leu
 2030 2035 2040

Glu Lys Ile Leu Ser Lys Gln Ser Gly His Arg Ala Asn Ala Asn
 2045 2050 2055

Asn Tyr Met Gly Gly Leu Thr Asn
 2060 2065

<210> SEQ ID NO 6
 <211> LENGTH: 609
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 6

Met Lys Lys Gln Ile Ile Ser Leu Gly Ala Leu Ala Val Ala Ser Ser
 1 5 10 15

Leu Phe Thr Trp Asp Asn Lys Ala Asp Ala Ile Val Thr Lys Asp Tyr
 20 25 30

Ser Lys Glu Ser Arg Val Asn Glu Asn Ser Lys Tyr Asp Thr Pro Ile
 35 40 45

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Pro Asp Trp Tyr Leu Gly Ser Ile Leu Asn Arg Leu Gly Asp Gln Ile
 50 55 60

Tyr Tyr Ala Lys Glu Leu Thr Asn Lys Tyr Glu Tyr Gly Glu Lys Glu
 65 70 75 80

Tyr Lys Gln Ala Ile Asp Lys Leu Met Thr Arg Val Leu Gly Glu Asp
 85 90 95

His Tyr Leu Leu Glu Lys Lys Lys Ala Gln Tyr Glu Ala Tyr Lys Lys
 100 105 110

Trp Phe Glu Lys His Lys Ser Glu Asn Pro His Ser Ser Leu Lys Lys
 115 120 125

Ile Lys Phe Asp Asp Phe Asp Leu Tyr Arg Leu Thr Lys Lys Glu Tyr
 130 135 140

Asn Glu Leu His Gln Ser Leu Lys Glu Ala Val Asp Glu Phe Asn Ser
 145 150 155 160

Glu Val Lys Asn Ile Gln Ser Lys Gln Lys Asp Leu Leu Pro Tyr Asp
 165 170 175

Glu Ala Thr Glu Asn Arg Val Thr Asn Gly Ile Tyr Asp Phe Val Cys
 180 185 190

Glu Ile Asp Thr Leu Tyr Ala Ala Tyr Phe Asn His Ser Gln Tyr Gly
 195 200 205

His Asn Ala Lys Glu Leu Arg Ala Lys Leu Asp Ile Ile Leu Gly Asp
 210 215 220

Ala Lys Asp Pro Val Arg Ile Thr Asn Glu Arg Ile Arg Lys Glu Met
 225 230 235 240

Met Asp Asp Leu Asn Ser Ile Ile Asp Asp Phe Phe Met Asp Thr Asn
 245 250 255

Met Asn Arg Pro Leu Asn Ile Thr Lys Phe Asn Pro Asn Ile His Asp
 260 265 270

Tyr Thr Asn Lys Pro Glu Asn Arg Asp Asn Phe Asp Lys Leu Val Lys
 275 280 285

Glu Thr Arg Glu Ala Ile Ala Asn Ala Asp Glu Ser Trp Lys Thr Arg
 290 295 300

Thr Val Lys Asn Tyr Gly Glu Ser Glu Thr Lys Ser Pro Val Val Lys
 305 310 315 320

Glu Glu Lys Lys Val Glu Glu Pro Gln Leu Pro Lys Val Gly Asn Gln
 325 330 335

Gln Glu Asp Lys Ile Thr Val Gly Thr Thr Glu Glu Ala Pro Leu Pro
 340 345 350

Ile Ala Gln Pro Leu Val Lys Ile Pro Gln Gly Thr Ile Gln Gly Glu
 355 360 365

Ile Val Lys Gly Pro Glu Tyr Leu Thr Met Glu Asn Lys Thr Leu Gln
 370 375 380

Gly Glu Ile Val Gln Gly Pro Asp Phe Pro Thr Met Glu Gln Asn Arg
 385 390 395 400

Pro Ser Leu Ser Asp Asn Tyr Thr Gln Pro Thr Thr Pro Asn Pro Ile
 405 410 415

Leu Lys Gly Ile Glu Gly Asn Ser Thr Lys Leu Glu Ile Lys Pro Gln
 420 425 430

Gly Thr Glu Ser Thr Leu Lys Gly Thr Gln Gly Glu Ser Ser Asp Ile
 435 440 445

Glu Val Lys Pro Gln Ala Thr Glu Thr Thr Glu Ala Ser His Tyr Pro
 450 455 460

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Ala Arg Pro Gln Phe Asn Lys Thr Pro Lys Tyr Val Lys Tyr Arg Asp
 465 470 475 480

Ala Gly Thr Gly Ile Arg Glu Tyr Asn Asp Gly Thr Phe Gly Tyr Glu
 485 490 495

Ala Arg Pro Arg Phe Asn Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val
 500 505 510

Thr Thr Asn Gln Asp Gly Thr Val Ser Tyr Gly Ala Arg Pro Thr Gln
 515 520 525

Asn Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val Thr Thr His Ala Asn
 530 535 540

Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr Gln Asn Lys Pro Ser Glu
 545 550 555 560

Thr Asn Ala Tyr Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr
 565 570 575

Gly Ala Arg Pro Thr Gln Asn Lys Pro Ser Lys Thr Asn Ala Tyr Asn
 580 585 590

Val Thr Thr His Ala Asp Gly Thr Ala Thr Tyr Gly Pro Arg Val Thr
 595 600 605

Lys

<210> SEQ ID NO 7
 <211> LENGTH: 144
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 7

Met Lys Lys Val Ile Gly Leu Leu Leu Val Ser Thr Leu Ala Leu Thr
 1 5 10 15

Ala Cys Gly Glu Lys Glu Lys Pro Lys Lys Glu Glu Asn Lys Lys Ser
 20 25 30

Gln Thr Gln Lys His Lys Asp Ser Lys Pro Lys Thr Gln Gln Glu Lys
 35 40 45

Met Lys Lys Val Glu Asp Lys Asn Pro Pro Asn Asn Ser Ile Gln Asn
 50 55 60

Asn Ser Asn Asn Gln Asn Gln Ser Gln Asn Asn Gln Leu Asn Asn Asn
 65 70 75 80

Ser Asp Pro Ser Asn Asn Thr Pro Ala Asn Ile Asn Lys Asn Asp Ser
 85 90 95

Gln Asn Thr Asn Leu Asn Asp Glu Tyr Val Val Ser Pro Gly Trp Thr
 100 105 110

Lys Asp Glu Gln Ala Lys Ala Phe Glu Glu Tyr Lys Lys Gly Lys Glu
 115 120 125

Asp Glu Ala Arg Ala Gly Ala Ser Ala Val Pro Gly Ala Asn Ile Asn
 130 135 140

<210> SEQ ID NO 8
 <211> LENGTH: 1257
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 8

Met Ala Lys Lys Phe Asn Tyr Lys Leu Pro Ser Met Val Ala Leu Thr
 1 5 10 15

Leu Val Gly Ser Ala Val Thr Ala His Gln Val Gln Ala Ala Glu Thr
 20 25 30

Thr Gln Asp Gln Thr Thr Asn Lys Asn Val Leu Asp Ser Asn Lys Val

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| 35 | | | | | 40 | | | | | 45 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Thr | Thr | Glu | Gln | Ala | Lys | Ala | Glu | Val | Lys | Asn | Pro | Thr | Gln |
| 50 | | | | | 55 | | | | | 60 | | | | | |
| Asn | Ile | Ser | Gly | Thr | Gln | Val | Tyr | Gln | Asp | Pro | Ala | Ile | Val | Gln | Pro |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Lys | Ala | Ala | Asn | Lys | Thr | Gly | Asn | Ala | Gln | Val | Asn | Gln | Lys | Val | Asp |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Thr | Gln | Val | Asn | Gly | Asp | Thr | Arg | Ala | Thr | Gln | Ser | Thr | Thr | Ser |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Asn | Asn | Ala | Lys | Pro | Val | Thr | Lys | Ser | Thr | Asn | Thr | Thr | Ala | Pro | Lys |
| | | | 115 | | | | | 120 | | | | | 125 | | |
| Thr | Asn | Asn | Asn | Val | Thr | Ser | Ala | Gly | Tyr | Ser | Leu | Val | Asp | Asp | Glu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asp | Asp | Asn | Ser | Glu | Asn | Gln | Ile | Asn | Pro | Glu | Leu | Ile | Lys | Ser | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Lys | Pro | Ala | Ala | Leu | Glu | Thr | Gln | Tyr | Lys | Ala | Ala | Ala | Pro | Lys |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Thr | Pro | Val | Ala | Pro | Lys | Ala | Lys | Thr | Glu | Ala | Thr | Pro | Lys | Val |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Thr | Thr | Phe | Ser | Ala | Ser | Ala | Gln | Pro | Arg | Ser | Ala | Ala | Ala | Ala | Pro |
| | | | 195 | | | | 200 | | | | | | 205 | | |
| Lys | Thr | Ser | Leu | Pro | Lys | Tyr | Lys | Pro | Gln | Val | Asn | Ser | Ser | Ile | Asn |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Tyr | Ile | Arg | Lys | Asn | Asn | Leu | Lys | Ala | Pro | Lys | Ile | Glu | Glu | Asp |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Tyr | Thr | Ser | Tyr | Phe | Pro | Lys | Tyr | Ala | Tyr | Arg | Asn | Gly | Val | Gly | Arg |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Pro | Glu | Gly | Ile | Val | Val | His | Asp | Thr | Ala | Asn | Asp | Arg | Ser | Thr | Ile |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Asn | Gly | Glu | Ile | Ser | Tyr | Met | Lys | Asn | Asn | Tyr | Gln | Asn | Ala | Phe | Val |
| | | 275 | | | | | 280 | | | | | | 285 | | |
| His | Ala | Phe | Val | Asp | Gly | Asp | Arg | Ile | Ile | Glu | Thr | Ala | Pro | Thr | Asp |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Tyr | Leu | Ser | Trp | Gly | Val | Gly | Ala | Val | Gly | Asn | Pro | Arg | Phe | Ile | Asn |
| | 305 | | | | | 310 | | | | | 315 | | | | 320 |
| Val | Glu | Ile | Val | His | Thr | His | Asp | Tyr | Ala | Ser | Phe | Ala | Arg | Ser | Met |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Asn | Asn | Tyr | Ala | Asp | Tyr | Ala | Ala | Thr | Gln | Leu | Gln | Tyr | Tyr | Gly | Leu |
| | | | 340 | | | | | 345 | | | | | | 350 | |
| Lys | Pro | Asp | Ser | Ala | Glu | Tyr | Asp | Gly | Asn | Gly | Thr | Val | Trp | Thr | His |
| | | 355 | | | | | 360 | | | | | | 365 | | |
| Tyr | Ala | Val | Ser | Lys | Tyr | Leu | Gly | Gly | Thr | Asp | His | Ala | Asp | Pro | His |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Gly | Tyr | Leu | Arg | Ser | His | Asn | Tyr | Ser | Tyr | Asp | Gln | Leu | Tyr | Asp | Leu |
| | 385 | | | | | 390 | | | | | 395 | | | | 400 |
| Ile | Asn | Glu | Lys | Tyr | Leu | Ile | Lys | Met | Gly | Lys | Val | Ala | Pro | Trp | Gly |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Thr | Gln | Ser | Thr | Thr | Thr | Pro | Thr | Thr | Pro | Ser | Lys | Pro | Ser | Thr | Pro |
| | | | | 420 | | | | | 425 | | | | | 430 | |
| Ser | Lys | Pro | Ser | Thr | Pro | Ser | Thr | Gly | Lys | Leu | Thr | Val | Ala | Ala | Asn |
| | | 435 | | | | | | 440 | | | | | 445 | | |
| Asn | Gly | Val | Ala | Gln | Ile | Lys | Pro | Thr | Asn | Ser | Gly | Leu | Tyr | Thr | Thr |
| | 450 | | | | | | 455 | | | | | | 460 | | |

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Val Tyr Asp Lys Thr Gly Lys Ala Thr Asn Glu Val Gln Lys Thr Phe
 465 470 475 480
 Ala Val Ser Lys Thr Ala Thr Leu Gly Asn Gln Lys Phe Tyr Leu Val
 485 490 495
 Gln Asp Tyr Asn Ser Gly Asn Lys Phe Gly Trp Val Lys Glu Gly Asp
 500 505 510
 Val Val Tyr Asn Thr Ala Lys Ser Pro Val Asn Val Asn Gln Ser Tyr
 515 520 525
 Ser Ile Lys Pro Gly Thr Lys Leu Tyr Thr Val Pro Trp Gly Thr Ser
 530 535 540
 Lys Gln Val Ala Gly Ser Val Ser Gly Ser Gly Asn Gln Thr Phe Lys
 545 550 555 560
 Ala Ser Lys Gln Gln Gln Ile Asp Lys Ser Ile Tyr Leu Tyr Gly Ser
 565 570 575
 Val Asn Gly Lys Ser Gly Trp Val Ser Lys Ala Tyr Leu Val Asp Thr
 580 585 590
 Ala Lys Pro Thr Pro Thr Pro Thr Pro Lys Pro Ser Thr Pro Thr Thr
 595 600 605
 Asn Asn Lys Leu Thr Val Ser Ser Leu Asn Gly Val Ala Gln Ile Asn
 610 615 620
 Ala Lys Asn Asn Gly Leu Phe Thr Thr Val Tyr Asp Lys Thr Gly Lys
 625 630 635 640
 Pro Thr Lys Glu Val Gln Lys Thr Phe Ala Val Thr Lys Glu Ala Ser
 645 650 655
 Leu Gly Gly Asn Lys Phe Tyr Leu Val Lys Asp Tyr Asn Ser Pro Thr
 660 665 670
 Leu Ile Gly Trp Val Lys Gln Gly Asp Val Ile Tyr Asn Asn Ala Lys
 675 680 685
 Ser Pro Val Asn Val Met Gln Thr Tyr Thr Val Lys Pro Gly Thr Lys
 690 695 700
 Leu Tyr Ser Val Pro Trp Gly Thr Tyr Lys Gln Glu Ala Gly Ala Val
 705 710 715 720
 Ser Gly Thr Gly Asn Gln Thr Phe Lys Ala Thr Lys Gln Gln Gln Ile
 725 730 735
 Asp Lys Ser Ile Tyr Leu Tyr Gly Thr Val Asn Gly Lys Ser Gly Trp
 740 745 750
 Ile Ser Lys Ala Tyr Leu Ala Val Pro Ala Ala Pro Lys Lys Ala Val
 755 760 765
 Ala Gln Pro Lys Thr Ala Val Lys Ala Tyr Ala Val Thr Lys Pro Gln
 770 775 780
 Thr Thr Gln Thr Val Ser Lys Ile Ala Gln Val Lys Pro Asn Asn Thr
 785 790 795 800
 Gly Ile Arg Ala Ser Val Tyr Glu Lys Thr Ala Lys Asn Gly Ala Lys
 805 810 815
 Tyr Ala Asp Arg Thr Phe Tyr Val Thr Lys Glu Arg Ala His Gly Asn
 820 825 830
 Glu Thr Tyr Val Leu Leu Asn Asn Thr Ser His Asn Ile Pro Leu Gly
 835 840 845
 Trp Phe Asn Val Lys Asp Leu Asn Val Gln Asn Leu Gly Lys Glu Val
 850 855 860
 Lys Thr Thr Gln Lys Tyr Thr Val Asn Arg Ser Asn Asn Gly Leu Ser
 865 870 875 880

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Met Val Pro Trp Gly Thr Lys Asn Gln Val Ile Leu Thr Gly Asn Asn
      885                               890                               895

Ile Ala Gln Gly Thr Phe Asn Ala Thr Lys Gln Val Ser Val Gly Lys
      900                               905                               910

Asp Val Tyr Leu Tyr Gly Thr Ile Asn Asn Arg Thr Gly Trp Val Asn
      915                               920                               925

Ser Lys Asp Leu Thr Ala Pro Thr Ala Val Lys Pro Thr Thr Ser Ala
      930                               935                               940

Ala Lys Asp Tyr Asn Tyr Thr Tyr Val Ile Lys Asn Gly Asn Gly Tyr
      945                               950                               955                               960

Tyr Tyr Val Thr Pro Asn Ser Asp Thr Ala Lys Tyr Ser Leu Lys Ala
      965                               970                               975

Phe Asn Glu Gln Pro Phe Ala Val Val Lys Glu Gln Val Ile Asn Gly
      980                               985                               990

Gln Thr Trp Tyr Tyr Gly Lys Leu Ser Asn Gly Lys Leu Ala Trp Ile
      995                               1000                               1005

Lys Ser Thr Asp Leu Ala Lys Glu Leu Ile Lys Tyr Asn Gln Ile
      1010                               1015                               1020

Gly Met Thr Leu Asn Gln Val Ala Gln Ile Gln Ala Gly Leu Gln
      1025                               1030                               1035

Tyr Lys Pro Gln Val Gln Arg Val Pro Gly Lys Trp Thr Asp Ala
      1040                               1045                               1050

Asn Phe Asn Asp Val Lys His Ala Met Asp Thr Lys Arg Leu Ala
      1055                               1060                               1065

Gln Asp Pro Ala Leu Lys Tyr Gln Phe Leu Arg Leu Asp Gln Pro
      1070                               1075                               1080

Gln Asn Ile Ser Ile Asp Lys Ile Asn Gln Phe Leu Lys Gly Lys
      1085                               1090                               1095

Gly Val Leu Glu Asn Gln Gly Ala Ala Phe Asn Lys Ala Ala Gln
      1100                               1105                               1110

Met Tyr Gly Ile Asn Glu Val Tyr Leu Ile Ser His Ala Leu Leu
      1115                               1120                               1125

Glu Thr Gly Asn Gly Thr Ser Gln Leu Ala Lys Gly Ala Asp Val
      1130                               1135                               1140

Val Asn Asn Lys Val Val Thr Asn Ser Asn Thr Lys Tyr His Asn
      1145                               1150                               1155

Val Phe Gly Ile Ala Ala Tyr Asp Asn Asp Pro Leu Arg Glu Gly
      1160                               1165                               1170

Ile Lys Tyr Ala Lys Gln Ala Gly Trp Asp Thr Val Ser Lys Ala
      1175                               1180                               1185

Ile Val Gly Gly Ala Lys Phe Ile Gly Asn Ser Tyr Val Lys Ala
      1190                               1195                               1200

Gly Gln Asn Thr Leu Tyr Lys Met Arg Trp Asn Pro Ala His Pro
      1205                               1210                               1215

Gly Thr His Gln Tyr Ala Thr Asp Val Asp Trp Ala Asn Ile Asn
      1220                               1225                               1230

Ala Lys Ile Ile Lys Gly Tyr Tyr Asp Lys Ile Gly Glu Val Gly
      1235                               1240                               1245

Lys Tyr Phe Asp Ile Pro Gln Tyr Lys
      1250                               1255

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<210> SEQ ID NO 9

<211> LENGTH: 486

<212> TYPE: PRT

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<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 9

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Met Ser Asn Asn Phe Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile
 1           5           10           15
Asp Thr Asn Ser His Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln
          20           25           30
Ser Glu Leu Glu His Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe
          35           40           45
Pro Pro Arg Asn Ala Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr
 50           55           60
Asn His Asn Lys Gln Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn
 65           70           75           80
Val Gln Asn Glu Ala Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser
          85           90           95
His Ser Thr Glu Ser Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln
          100          105          110
His Glu Glu Gly Tyr Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser
          115          120          125
His Pro Glu Pro Ile Glu Asp Asn Asp Lys His Glu Thr Ile Lys Glu
          130          135          140
Ala Glu Asn Asn Thr Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala
          145          150          155          160
Glu Gln Ser Gln Gln Pro Lys Pro Tyr Phe Ala Thr Gly Ala Asn Gln
          165          170          175
Ala Asn Thr Ser Lys Asp Lys His Asp Asp Val Thr Val Lys Gln Asp
          180          185          190
Lys Asp Glu Ser Lys Asp His His Ser Gly Lys Lys Gly Ala Ala Ile
          195          200          205
Gly Ala Gly Thr Ala Gly Val Ala Gly Ala Ala Gly Ala Met Gly Val
          210          215          220
Ser Lys Ala Lys Lys His Ser Asn Asp Ala Gln Asn Lys Ser Asn Ser
          225          230          235          240
Gly Lys Val Asn Asn Ser Thr Glu Asp Lys Ala Ser Glu Asp Lys Ser
          245          250          255
Lys Glu His His Asn Gly Lys Lys Gly Ala Ala Ile Gly Ala Gly Thr
          260          265          270
Ala Gly Leu Ala Gly Gly Ala Ala Ser Asn Ser Ala Ser Ala Ala Ser
          275          280          285
Lys Pro His Ala Ser Asn Asn Ala Ser Gln Asn Asn Asp Glu His Asp
          290          295          300
His His Asp Arg Asp Lys Glu Arg Lys Lys Gly Gly Met Ala Lys Val
          305          310          315          320
Leu Leu Pro Leu Ile Ala Ala Val Leu Ile Ile Gly Ala Leu Ala Ile
          325          330          335
Phe Gly Gly Met Ala Leu Asn Asn His Asn Asn Gly Thr Lys Glu Asn
          340          345          350
Lys Ile Ala Asn Thr Asn Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys
          355          360          365
Asp Thr Ser Lys Asp Ala Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser
          370          375          380
Asp Lys Ser Lys Asp Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp
          385          390          395          400

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Asn Asp Gln Asn Asn Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn
 405 410 415

Gln Asn Gln Gln Gln Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg
 420 425 430

Gln Gly Gly Gly Gln Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr
 435 440 445

Arg Ile Ala Ile Gln Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu
 450 455 460

Lys Ile Arg Arg Ala Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly
 465 470 475 480

Gln Gln Ile Val Ile Pro
 485

<210> SEQ ID NO 10
 <211> LENGTH: 1274
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 10

Met Ser Trp Phe Asp Lys Leu Phe Gly Glu Asp Asn Asp Ser Asn Asp
 1 5 10 15

Asp Leu Ile His Arg Lys Lys Lys Arg Arg Gln Glu Ser Gln Asn Ile
 20 25 30

Asp Asn Asp His Asp Ser Leu Leu Pro Gln Asn Asn Asp Ile Tyr Ser
 35 40 45

Arg Pro Arg Gly Lys Phe Arg Phe Pro Met Ser Val Ala Tyr Glu Asn
 50 55 60

Glu Asn Val Glu Gln Ser Ala Asp Thr Ile Ser Asp Glu Lys Glu Gln
 65 70 75 80

Tyr His Arg Asp Tyr Arg Lys Gln Ser His Asp Ser Arg Ser Gln Lys
 85 90 95

Arg His Arg Arg Arg Arg Asn Gln Thr Thr Glu Glu Gln Asn Tyr Ser
 100 105 110

Glu Gln Arg Gly Asn Ser Lys Ile Ser Gln Gln Ser Ile Lys Tyr Lys
 115 120 125

Asp His Ser His Tyr His Thr Asn Lys Pro Gly Thr Tyr Val Ser Ala
 130 135 140

Ile Asn Gly Ile Glu Lys Glu Thr His Lys Ser Lys Thr His Asn Ile
 145 150 155 160

Tyr Ser Asn Asn Thr Asn His Arg Ala Lys Asp Ser Thr Thr Asp Tyr
 165 170 175

His Lys Glu Ser Phe Lys Thr Ser Glu Val Pro Ser Ala Ile Phe Gly
 180 185 190

Thr Met Lys Pro Lys Lys Leu Glu Asn Gly Arg Ile Pro Val Ser Lys
 195 200 205

Ser Ser Glu Lys Val Glu Ser Asp Lys Gln Lys Tyr Asp Lys Tyr Val
 210 215 220

Ala Lys Thr Gln Thr Ser Gln Asn Lys His Leu Glu Gln Glu Lys Gln
 225 230 235 240

Lys Asp Ser Val Val Lys Gln Gly Thr Ala Ser Lys Ser Ser Asp Glu
 245 250 255

Asn Val Ser Ser Thr Thr Lys Ser Thr Pro Asn Tyr Ser Lys Val Asp
 260 265 270

Asn Thr Ile Lys Ile Glu Asn Ile Tyr Ala Ser Gln Ile Val Glu Glu
 275 280 285

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Ile Arg Arg Glu Arg Glu Arg Lys Val Leu Gln Lys Arg Arg Phe Lys
 290 295 300
 Lys Ala Leu Gln Gln Lys Arg Glu Glu His Lys Asn Glu Glu Gln Asp
 305 310 315 320
 Ala Ile Gln Arg Ala Ile Asp Glu Met Tyr Ala Lys Gln Ala Glu Arg
 325 330 335
 Tyr Val Gly Asp Ser Ser Leu Asn Asp Asp Ser Asp Leu Thr Asp Asn
 340 345 350
 Ser Thr Glu Ala Ser Gln Leu His Thr Asn Glu Ile Glu Asp Glu Ala
 355 360 365
 Val Ser Asn Asp Glu Asn Lys Lys Ala Ser Ile Gln Asn Glu Asp Thr
 370 375 380
 Asp Asp Thr His Val Asp Glu Ser Pro Tyr Asn Tyr Glu Glu Val Ser
 385 390 395 400
 Leu Asn Gln Val Ser Thr Thr Lys Gln Leu Ser Asp Asp Glu Val Thr
 405 410 415
 Val Ser Asp Val Thr Ser Gln Arg Gln Ser Ala Leu Gln His Asn Val
 420 425 430
 Glu Val Asn Asn Gln Asp Glu Leu Lys Asn Gln Ser Arg Leu Ile Ala
 435 440 445
 Asp Ser Glu Glu Asp Gly Ala Thr Asn Glu Glu Glu Tyr Ser Gly Ser
 450 455 460
 Gln Ile Asp Asp Ala Glu Phe Tyr Glu Leu Asn Asp Thr Glu Val Asp
 465 470 475 480
 Glu Asp Thr Thr Ser Asn Ser Glu Asp Asn Thr Asn Arg Asp Ala Ser
 485 490 495
 Glu Met His Val Asp Ala Pro Lys Thr Gln Glu His Ala Val Thr Glu
 500 505 510
 Ser Gln Val Asn Asn Ile Asp Lys Thr Val Asp Asn Glu Ile Glu Leu
 515 520 525
 Ala Pro Arg His Lys Lys Asp Asp Gln Thr Asn Leu Ser Val Asn Ser
 530 535 540
 Leu Lys Thr Asn Asp Val Asn Asp Gly His Val Val Glu Asp Ser Ser
 545 550 555 560
 Met Asn Glu Ile Glu Lys Gln Asn Ala Glu Ile Thr Glu Asn Val Gln
 565 570 575
 Asn Glu Ala Ala Glu Ser Lys Gln Asn Val Glu Glu Lys Thr Ile Glu
 580 585 590
 Asn Val Asn Pro Lys Lys Gln Thr Glu Lys Val Ser Thr Leu Ser Lys
 595 600 605
 Arg Pro Phe Asn Val Val Met Thr Pro Ser Asp Lys Lys Arg Met Met
 610 615 620
 Asp Arg Lys Lys His Ser Lys Val Asn Val Pro Glu Leu Lys Pro Val
 625 630 635 640
 Gln Ser Lys Gln Ala Ala Ser Glu Ser Lys Thr Ala Thr Gln Asn Thr
 645 650 655
 Pro Ser Ser Ser Thr Asp Ser Gln Glu Ser Asn Thr Asn Ala Tyr Lys
 660 665 670
 Thr Asn Asn Met Thr Ser Asn Asn Val Glu Asn Asn Gln Leu Ile Gly
 675 680 685
 His Ala Ala Thr Glu Asn Asp Tyr Gln Asn Ala Gln Gln Tyr Ser Glu
 690 695 700

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Gln Lys Pro Ser Ala Asp Ser Thr Gln Thr Glu Ile Phe Glu Glu Ser
 705 710 715 720
 Gln Asp Asp Asn Gln Leu Glu Asn Glu Gln Val Asp Gln Ser Thr Ser
 725 730 735
 Ser Ser Val Ser Glu Val Ser Asp Ile Thr Glu Glu Ser Glu Glu Thr
 740 745 750
 Thr His Gln Asn Asn Thr Ser Gly Gln Gln Asp Asn Asp Asp Gln Gln
 755 760 765
 Lys Asp Leu Gln Leu Ser Phe Ser Asn Gln Asn Glu Asp Thr Ala Asn
 770 775 780
 Glu Asn Arg Pro Arg Thr Asn Gln Pro Asp Val Ala Thr Asn Gln Ala
 785 790 795 800
 Val Gln Thr Ser Lys Pro Met Ile Arg Lys Gly Pro Asn Ile Lys Leu
 805 810 815
 Pro Ser Val Ser Leu Leu Glu Glu Pro Gln Val Ile Glu Pro Asp Glu
 820 825 830
 Asp Trp Ile Thr Asp Lys Lys Lys Glu Leu Asn Asp Ala Leu Phe Tyr
 835 840 845
 Phe Asn Val Pro Ala Glu Val Gln Asp Val Thr Glu Gly Pro Ser Val
 850 855 860
 Thr Arg Phe Glu Leu Ser Val Glu Lys Gly Val Lys Val Ser Arg Ile
 865 870 875 880
 Thr Ala Leu Gln Asp Asp Ile Lys Met Ala Leu Ala Ala Lys Asp Ile
 885 890 895
 Arg Ile Glu Ala Pro Ile Pro Gly Thr Ser Arg Val Gly Ile Glu Val
 900 905 910
 Pro Asn Gln Asn Pro Thr Thr Val Asn Leu Arg Ser Ile Ile Glu Ser
 915 920 925
 Pro Ser Phe Lys Asn Ala Glu Ser Lys Leu Thr Val Ala Met Gly Tyr
 930 935 940
 Arg Ile Asn Asn Glu Pro Leu Leu Met Asp Ile Ala Lys Thr Pro His
 945 950 955 960
 Ala Leu Ile Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Ile Asn
 965 970 975
 Ser Ile Leu Met Ser Leu Leu Tyr Lys Asn His Pro Glu Glu Leu Arg
 980 985 990
 Leu Leu Leu Ile Asp Pro Lys Met Val Glu Leu Ala Pro Tyr Asn Gly
 995 1000 1005
 Leu Pro His Leu Val Ala Pro Val Ile Thr Asp Val Lys Ala Ala
 1010 1015 1020
 Thr Gln Ser Leu Lys Trp Ala Val Glu Glu Met Glu Arg Arg Tyr
 1025 1030 1035
 Lys Leu Phe Ala His Tyr His Val Arg Asn Ile Thr Ala Phe Asn
 1040 1045 1050
 Lys Lys Ala Pro Tyr Asp Glu Arg Met Pro Lys Ile Val Ile Val
 1055 1060 1065
 Ile Asp Glu Leu Ala Asp Leu Met Met Met Ala Pro Gln Glu Val
 1070 1075 1080
 Glu Gln Ser Ile Ala Arg Ile Ala Gln Lys Ala Arg Ala Cys Gly
 1085 1090 1095
 Ile His Met Leu Val Ala Thr Gln Arg Pro Ser Val Asn Val Ile
 1100 1105 1110
 Thr Gly Leu Ile Lys Ala Asn Ile Pro Thr Arg Ile Ala Phe Met

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Lys

<210> SEQ ID NO 12
 <211> LENGTH: 190
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 12

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Met Lys Leu Lys Ser Leu Ala Val Leu Ser Met Ser Ala Val Val Leu
 1           5           10           15
Thr Ala Cys Gly Asn Asp Thr Pro Lys Asp Glu Thr Lys Ser Thr Glu
 20           25           30
Ser Asn Thr Asn Gln Asp Thr Asn Thr Thr Lys Asp Val Ile Ala Leu
 35           40           45
Lys Asp Val Lys Thr Ser Pro Glu Asp Ala Val Lys Lys Ala Glu Glu
 50           55           60
Thr Tyr Lys Gly Gln Lys Leu Lys Gly Ile Ser Phe Glu Asn Ser Asn
 65           70           75           80
Gly Glu Trp Ala Tyr Lys Val Thr Gln Gln Lys Ser Gly Glu Glu Ser
 85           90           95
Glu Val Leu Val Asp Asp Lys Asn Lys Lys Val Ile Asn Lys Lys Thr
 100          105          110
Glu Lys Glu Asp Thr Val Asn Glu Asn Asp Asn Phe Lys Tyr Ser Asp
 115          120          125
Ala Ile Asp Tyr Lys Lys Ala Ile Lys Glu Gly Gln Lys Glu Phe Asp
 130          135          140
Gly Asp Ile Lys Glu Trp Ser Leu Glu Lys Asp Asp Gly Lys Leu Val
 145          150          155          160
Tyr Asn Ile Asp Leu Lys Lys Gly Asn Lys Lys Gln Glu Val Thr Val
 165          170          175
Asp Ala Lys Asn Gly Lys Val Leu Lys Ser Glu Gln Asp Gln
 180          185          190

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<210> SEQ ID NO 13
 <211> LENGTH: 1009
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 13

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Met Lys Lys Lys Asn Trp Ile Tyr Ala Leu Ile Val Thr Leu Ile Ile
 1           5           10           15
Ile Ile Ala Ile Val Ser Met Ile Phe Phe Val Gln Thr Lys Tyr Gly
 20           25           30
Asp Gln Ser Glu Lys Gly Ser Gln Ser Val Ser Asn Lys Asn Asn Lys
 35           40           45
Ile His Ile Ala Ile Val Asn Glu Asp Gln Pro Thr Thr Tyr Asn Gly
 50           55           60
Lys Lys Val Glu Leu Gly Gln Ala Phe Ile Lys Arg Leu Ala Asn Glu
 65           70           75           80
Lys Asn Tyr Lys Phe Glu Thr Val Thr Arg Asn Val Ala Glu Ser Gly
 85           90           95
Leu Lys Asn Gly Gly Tyr Gln Val Met Ile Val Ile Pro Glu Asn Phe
 100          105          110
Ser Lys Leu Ala Met Gln Leu Asp Ala Lys Thr Pro Ser Lys Ile Ser
 115          120          125
Leu Gln Tyr Lys Thr Ala Val Gly Gln Lys Glu Glu Val Ala Lys Asn

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| 130 | | | | | 135 | | | | | 140 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Glu | Lys | Val | Val | Ser | Asn | Val | Leu | Asn | Asp | Phe | Asn | Lys | Asn | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Val | Glu | Ile | Tyr | Leu | Thr | Ser | Ile | Ile | Asp | Asn | Leu | His | Asn | Ala | Gln |
| | | | | 165 | | | | | 170 | | | | | | 175 |
| Lys | Asn | Val | Gly | Ala | Ile | Met | Thr | Arg | Glu | His | Gly | Val | Asn | Ser | Lys |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Phe | Ser | Asn | Tyr | Leu | Leu | Asn | Pro | Ile | Asn | Asp | Phe | Pro | Glu | Leu | Phe |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Asp | Thr | Leu | Val | Asn | Ser | Ile | Ser | Ala | Asn | Lys | Asp | Ile | Thr | Lys |
| | 210 | | | | | 215 | | | | | | 220 | | | |
| Trp | Phe | Gln | Thr | Tyr | Asn | Lys | Ser | Leu | Leu | Ser | Ala | Asn | Ser | Asp | Thr |
| | 225 | | | | 230 | | | | | | 235 | | | | 240 |
| Phe | Arg | Val | Asn | Thr | Asp | Tyr | Asn | Val | Ser | Thr | Leu | Ile | Glu | Lys | Gln |
| | | | | 245 | | | | | 250 | | | | | | 255 |
| Asn | Ser | Leu | Phe | Asp | Glu | His | Asn | Thr | Ala | Met | Asp | Lys | Met | Leu | Gln |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Asp | Tyr | Lys | Ser | Gln | Lys | Asp | Ser | Val | Glu | Leu | Asp | Asn | Tyr | Ile | Asn |
| | | 275 | | | | | 280 | | | | | | 285 | | |
| Ala | Leu | Lys | Gln | Met | Asp | Ser | Gln | Ile | Asp | Gln | Gln | Ser | Ser | Met | Gln |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asp | Thr | Gly | Lys | Glu | Glu | Tyr | Lys | Gln | Thr | Val | Lys | Glu | Asn | Leu | Asp |
| | 305 | | | | | 310 | | | | | 315 | | | | 320 |
| Lys | Leu | Arg | Glu | Ile | Ile | Gln | Ser | Gln | Glu | Ser | Pro | Phe | Ser | Lys | Gly |
| | | | | 325 | | | | | 330 | | | | | | 335 |
| Met | Ile | Glu | Asp | Tyr | Arg | Lys | Gln | Leu | Thr | Glu | Ser | Leu | Gln | Asp | Glu |
| | | | 340 | | | | | 345 | | | | | | 350 | |
| Leu | Ala | Asn | Asn | Lys | Asp | Leu | Gln | Asp | Ala | Leu | Asn | Ser | Ile | Lys | Met |
| | | 355 | | | | | 360 | | | | | | 365 | | |
| Asn | Asn | Ala | Gln | Phe | Ala | Glu | Asn | Leu | Glu | Lys | Gln | Leu | His | Asp | Asp |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ile | Val | Lys | Glu | Pro | Asp | Ser | Asp | Thr | Thr | Phe | Ile | Tyr | Asn | Met | Ser |
| | 385 | | | | 390 | | | | | | 395 | | | | 400 |
| Lys | Gln | Asp | Phe | Ile | Ala | Ala | Gly | Leu | Asn | Glu | Asp | Glu | Ala | Asn | Lys |
| | | | | 405 | | | | | 410 | | | | | | 415 |
| Tyr | Glu | Ala | Ile | Val | Lys | Glu | Ala | Lys | Arg | Tyr | Lys | Asn | Glu | Tyr | Asn |
| | | 420 | | | | | | 425 | | | | | | 430 | |
| Leu | Lys | Lys | Pro | Leu | Ala | Glu | His | Ile | Asn | Leu | Thr | Asp | Tyr | Asp | Asn |
| | | 435 | | | | | 440 | | | | | | 445 | | |
| Gln | Val | Ala | Gln | Asp | Thr | Ser | Ser | Leu | Ile | Asn | Asp | Gly | Val | Lys | Val |
| | 450 | | | | | 455 | | | | | | 460 | | | |
| Gln | Arg | Thr | Glu | Thr | Ile | Lys | Ser | Asn | Asp | Ile | Asn | Gln | Leu | Thr | Val |
| | 465 | | | | 470 | | | | | 475 | | | | | 480 |
| Ala | Thr | Asp | Pro | His | Phe | Asn | Phe | Glu | Gly | Asp | Ile | Lys | Ile | Asn | Gly |
| | | | | 485 | | | | | 490 | | | | | | 495 |
| Lys | Lys | Tyr | Asp | Ile | Lys | Asp | Gln | Ser | Val | Gln | Leu | Asp | Thr | Ser | Asn |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Lys | Glu | Tyr | Lys | Val | Glu | Val | Asn | Gly | Val | Ala | Lys | Leu | Lys | Lys | Asp |
| | | 515 | | | | | 520 | | | | | | 525 | | |
| Ala | Glu | Lys | Asp | Phe | Leu | Lys | Asp | Lys | Thr | Met | His | Leu | Gln | Leu | Leu |
| | 530 | | | | | | 535 | | | | | 540 | | | |
| Phe | Gly | Gln | Ala | Asn | Arg | Gln | Asp | Glu | Pro | Asn | Asp | Lys | Lys | Ala | Thr |
| | 545 | | | | 550 | | | | | | 555 | | | | 560 |

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His Pro Ile Gly Leu Ala Leu Val Ile Leu Thr Val Leu Val Ile Ile
      980                               985           990

Gly Phe Val Leu Asn Met Phe Ile Lys His Phe Lys Lys Glu Arg Leu
      995                               1000          1005

Ile

<210> SEQ ID NO 14
<211> LENGTH: 396
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 14

Met Thr Gln Gln Gln Asn Asn Lys Arg Thr Leu Lys Asn Lys His Thr
 1      5      10      15

Tyr Gln Asn Glu Pro Leu Pro Asn Arg Lys Asp Phe Val Val Ser Phe
 20      25      30

Ile Thr Gly Ala Leu Val Gly Ser Ala Leu Gly Leu Tyr Phe Lys Asn
 35      40      45

Lys Val Tyr Gln Lys Ala Asp Asp Leu Lys Val Lys Glu Gln Glu Leu
 50      55      60

Ser Gln Lys Phe Glu Glu Arg Lys Thr Gln Leu Glu Glu Thr Val Ala
 65      70      75      80

Phe Thr Lys Glu Arg Val Glu Gly Phe Leu Asn Lys Ser Lys Asn Glu
 85      90      95

Gln Ala Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser
 100     105     110

Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu
 115     120     125

Ala Lys Arg Glu Ala Gln Thr Glu Thr Asp Lys Ser Ala Ala Val Ser
 130     135     140

Asn Glu Glu Ser Lys Ala Ser Ala Leu Lys Ala Gln Gln Ala Ala Ile
 145     150     155     160

Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala
 165     170     175

Gln Ala Ile Gln Glu Val Lys Lys Glu Ala Gln Ala Glu Thr Asp Lys
 180     185     190

Ser Ala Asp Val Ser Asn Glu Glu Ser Lys Ala Ser Thr Leu Asn Val
 195     200     205

Ser Lys Glu Glu Ser Gln Ala Glu Arg Leu Ala Asn Ala Ala Lys Gln
 210     215     220

Lys Gln Ala Lys Leu Thr Pro Gly Ser Lys Glu Ser Gln Leu Thr Glu
 225     230     235     240

Ala Leu Phe Ala Glu Lys Pro Val Ala Lys Asn Asp Leu Lys Glu Ile
 245     250     255

Pro Leu Leu Val Thr Lys Lys Asn Asp Val Ser Glu Thr Val Asn Thr
 260     265     270

Asp Asn Lys Asp Thr Val Lys Gln Lys Glu Ala Lys Phe Glu Asn Gly
 275     280     285

Val Ile Thr Arg Lys Ala Asp Glu Lys Thr Pro Asn Asn Thr Ala Val
 290     295     300

Asp Lys Lys Ser Gly Lys Gln Ser Lys Lys Thr Thr Pro Ser Asn Lys
 305     310     315     320

Arg Asn Ala Ser Lys Ala Ser Thr Asn Lys Thr Ser Gly Gln Lys Lys
 325     330     335

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Gln His Asn Lys Lys Ala Ser Gln Gly Ala Lys Lys Gln Ser Ser Ser
 340 345 350

Ser Asn Ser Thr Thr Lys Thr Asn Gln Lys Asn Ser Lys Ala Thr Asn
 355 360 365

Ala Lys Ser Ser Asn Ala Ser Lys Lys Ser Asn Ala Lys Val Glu Lys
 370 375 380

Ala Lys Ser Lys Ile Glu Lys Arg Thr Phe Asn Asp
 385 390 395

<210> SEQ ID NO 15
 <211> LENGTH: 769
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 15

Met Asp Ile Gly Lys Lys His Val Ile Pro Lys Ser Gln Tyr Arg Arg
 1 5 10 15

Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg Glu Glu Asn Leu Asn
 20 25 30

Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr Thr Ser Lys Lys Ala
 35 40 45

Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys His Glu Arg Phe Lys
 50 55 60

Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn Arg Asp Val Asn Glu
 65 70 75 80

Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Gly Ser Lys Ser Ala Tyr
 85 90 95

Asn Lys Asp His Tyr Leu Thr Asp Asp Val Ser Lys Lys Gln Asn Ser
 100 105 110

Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser Lys Tyr Tyr Glu Gln
 115 120 125

Asn Thr Glu Ala Thr Leu Ser Thr Asn Ser Thr Asp Lys Val Glu Ser
 130 135 140

Thr Asp Met Arg Lys Leu Ser Ser Asp Lys Asn Lys Val Gly His Glu
 145 150 155 160

Glu Gln His Val Leu Ser Lys Pro Ser Glu His Asp Lys Glu Thr Arg
 165 170 175

Ile Asp Phe Glu Ser Ser Arg Thr Asp Ser Asp Ser Ser Met Gln Thr
 180 185 190

Glu Lys Ile Lys Lys Asp Ser Ser Asp Gly Asn Lys Ser Ser Asn Leu
 195 200 205

Lys Ser Glu Val Ile Ser Asp Lys Ser Asn Ser Val Pro Ile Leu Ser
 210 215 220

Glu Ser Asp Asp Glu Val Asn Asn Gln Lys Pro Leu Thr Leu Pro Glu
 225 230 235 240

Glu Gln Lys Leu Lys Arg Gln Gln Ser Gln Asn Glu Gln Thr Lys Thr
 245 250 255

Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys Ser Asn His Glu Asn
 260 265 270

Asp Leu Ser His His Thr Pro Ser Ile Ser Asp Asp Lys Asp Tyr Val
 275 280 285

Met Arg Glu Asp His Ile Val Asp Asp Asn Pro Asp Asn Asp Ile Asn
 290 295 300

Thr Pro Ser Leu Ser Lys Ile Asp Asp Asp Arg Lys Leu Asp Glu Lys
 305 310 315 320

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Phe Arg Gln Ile Ile Phe Ser His Lys Asp Asp Leu Lys Ser Ile Thr
740 745 750

Ala Lys Ile Tyr Arg Asp Gly Lys Glu Lys Glu Ile Asn Ile Lys Leu
755 760 765

Lys

<210> SEQ ID NO 16

<211> LENGTH: 208

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 16

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
1 5 10 15

Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
20 25 30

Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
35 40 45

Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
50 55 60

Asp Tyr Lys Ala Arg Gly Ala Asn Glu Asn Gln Thr Leu Asn Tyr Lys
65 70 75 80

Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
85 90 95

Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
100 105 110

Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
130 135 140

Pro Gly Met Asn Asp Gln Ala Glu Met Asp Asn Glu Ser Glu Asp Ile
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Leu Pro
165 170 175

Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
180 185 190

Glu Lys His Asp Asn Arg Glu Asn Asn Ser Ala Glu Thr Lys Val Lys
195 200 205

<210> SEQ ID NO 17

<211> LENGTH: 227

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 17

Met Asp Lys Lys Lys Val Ile Lys Phe Met Ile Asn Val Leu Pro Ile
1 5 10 15

Val Leu Val Pro Leu Ile Val Glu Arg Lys Arg Ile Lys Gln His Pro
20 25 30

Asp Val Gln Lys Val Thr Asp Ala Thr Ser Lys Val Ala Ser Lys Thr
35 40 45

Ser Ala Ala Ile Ser Asn Thr Ala Ser Asp Val Lys Glu Tyr Val Gly
50 55 60

Asp Lys Lys Gln Asp Phe Glu Asn Lys Arg Glu Leu Lys Lys Phe Ala
65 70 75 80

Arg Glu His Asp Pro Ala Tyr Ile Glu Lys Lys Gly Glu Lys Leu Ala

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 85 | | 90 | | 95 | | | | | | | | | | |
| Lys | Gln | Asn | Arg | Lys | Asp | Ala | Asp | Lys | Met | Asn | Lys | Ile | Leu | Gln | Lys |
| | 100 | | | | | | 105 | | | | | | 110 | | |
| Asn | Ile | Glu | Lys | Arg | His | Lys | Glu | Glu | Gln | Lys | Ala | Arg | Glu | Lys | Asn |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| Glu | Ile | Gln | Arg | Ile | Lys | Asp | Met | Lys | Lys | Ser | Gln | Lys | Tyr | Glu | Val |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Ala | Gly | Leu | Thr | Pro | Asn | Lys | Leu | Asp | Glu | Lys | Thr | Glu | Lys | Lys |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Gly | Asp | Lys | Leu | Ala | Glu | Lys | Asn | Arg | Lys | Glu | Ile | Ala | Lys | Met | Asn |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Lys | Lys | Leu | Gln | Lys | Asn | Ile | Glu | Lys | Arg | His | Lys | Glu | Glu | Gln | Lys |
| | | 180 | | | | | | 185 | | | | | | 190 | |
| Arg | Gln | Gln | Glu | Ala | Asp | Lys | Ala | Arg | Ile | Lys | Ser | Phe | Lys | Lys | Tyr |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Lys | Asp | Tyr | Val | Ala | Lys | Ser | Ala | Ser | Gln | Gln | Asn | Lys | Glu | Asn | Asn |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Glu | Ala | | | | | | | | | | | | | |
| | 225 | | | | | | | | | | | | | | |

<210> SEQ ID NO 18
 <211> LENGTH: 404
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 18

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Tyr | His | Trp | Phe | Lys | Lys | Met | Leu | Leu | Ser | Thr | Ser | Met | Leu |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Ile | Leu | Ser | Ser | Ser | Ser | Ser | Leu | Gly | Leu | Ala | Thr | His | Thr | Val | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Lys | Asp | Asn | Leu | Asn | Gly | Glu | Lys | Pro | Thr | Thr | Asn | Leu | Asn | His |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Asn | Val | Thr | Ser | Pro | Ser | Val | Asn | Ser | Glu | Met | Asn | Asn | Asn | Glu | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Thr | Pro | His | Glu | Ser | Asn | Gln | Ala | Gly | Asn | Glu | Gly | Thr | Gly | Ser |
| | 65 | | | 70 | | | | | 75 | | | | | 80 | |
| Asn | Ser | Arg | Asp | Ala | Asn | Pro | Asp | Ser | Asn | Asn | Val | Lys | Pro | Asp | Ser |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Asn | Asn | Gln | Asn | Pro | Ser | Pro | Asp | Ser | Lys | Pro | Asp | Pro | Asn | Asn | Pro |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asn | Pro | Gly | Pro | Asn | Pro | Lys | Pro | Asp | Pro | Asp | Lys | Pro | Lys | Pro | Asn |
| | | 115 | | | | 120 | | | | | 125 | | | | |
| Pro | Glu | Pro | Lys | Pro | Asp | Pro | Asp | Lys | Pro | Lys | Pro | Asn | Pro | Asp | Pro |
| | 130 | | | | 135 | | | | | | 140 | | | | |
| Lys | Pro | Asp | Pro | Asp | Lys | Pro | Lys | Pro | Asn | Pro | Asp | Pro | Lys | Pro | Asp |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Pro | Asn | Pro | Asn | Pro | Asn | Pro | Lys | Pro | Asp | Pro | Asn | Lys | Pro | Asn | Pro |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Asn | Pro | Ser | Pro | Asn | Pro | Asn | Gln | Pro | Gly | Asp | Ser | Asn | Gln | Ser | Gly |
| | | | 180 | | | | | 185 | | | | | | 190 | |
| Gly | Ser | Lys | Asn | Gly | Gly | Thr | Trp | Asn | Pro | Asn | Ala | Ser | Asp | Gly | Ser |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Asn | Gln | Gly | Gln | Trp | Gln | Pro | Asn | Gly | Asn | Gln | Gly | Asn | Ser | Gln | Asn |
| | 210 | | | | | 215 | | | | | 220 | | | | |

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Pro Thr Gly Asn Asp Phe Val Ser Gln Arg Phe Leu Ala Leu Ala Asn
225                230                235                240

Gly Ala Tyr Lys Tyr Asn Pro Tyr Ile Leu Asn Gln Ile Asn Gln Leu
                245                250                255

Gly Lys Glu Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile Ile
                260                265                270

Arg Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln Gln
                275                280                285

Gln Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser Glu
                290                295                300

Arg Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr Gly
305                310                315

Glu Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro Asp
                325                330                335

Ser Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr Val
                340                345                350

Val Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr Ser
                355                360                365

Lys Ser Trp Leu Ala Ile Val Cys Ser Met Met Val Val Phe Ser Ile
370                375                380

Met Leu Phe Leu Phe Val Lys Arg Asn Lys Lys Lys Asn Lys Asn Glu
385                390                395                400

Ser Gln Arg Arg

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<210> SEQ ID NO 19

<211> LENGTH: 231

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 19

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Met Lys Lys Thr Leu Leu Ala Ser Ser Leu Ala Val Gly Leu Gly Ile
1                5                10                15

Val Ala Gly Asn Ala Gly His Glu Ala Gln Ala Ser Glu Ala Asp Leu
                20                25                30

Asn Lys Ala Ser Leu Ala Gln Met Ala Gln Ser Asn Asp Gln Thr Leu
                35                40                45

Asn Gln Lys Pro Ile Glu Ala Gly Ala Tyr Asn Tyr Thr Phe Asp Tyr
50                55                60

Glu Gly Phe Thr Tyr His Phe Glu Ser Asp Gly Thr His Phe Ala Trp
65                70                75                80

Asn Tyr His Ala Thr Gly Ala Asn Gly Ala Asp Met Ser Ala Gln Ala
                85                90                95

Pro Ala Thr Asn Asn Val Ala Pro Ser Ala Asp Gln Ser Asn Gln Val
                100                105                110

Gln Ser Gln Glu Val Glu Ala Pro Gln Asn Ala Gln Thr Gln Gln Pro
                115                120                125

Gln Ala Ser Thr Ser Asn Asn Ser Gln Val Thr Ala Thr Pro Thr Glu
130                135                140

Ser Lys Ala Ser Glu Gly Ser Ser Val Asn Val Asn Asp His Leu Lys
145                150                155                160

Gln Ile Ala Gln Arg Glu Ser Gly Gly Asn Ile His Ala Val Asn Pro
                165                170                175

Thr Ser Gly Ala Ala Gly Lys Tyr Gln Phe Leu Gln Ser Thr Trp Asp
180                185                190

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Ser Val Ala Pro Ala Lys Tyr Lys Gly Val Ser Pro Ala Asn Ala Pro
 195 200 205

Glu Ser Val Gln Asp Ala Ala Ala Val Lys Leu Tyr Asn Thr Gly Gly
 210 215 220

Ala Gly His Trp Val Thr Ala
 225 230

<210> SEQ ID NO 20
 <211> LENGTH: 465
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 20

atgaaaagat tgtaggtttt attattagtg agcacggttag tgtaagtgc atgtggaat 60
 gatgagaatc aggaagaatc taaaaagaa gttaaatcaa aagaaaagaa aattgagaag 120
 gaaaaggaaa ataatcgaa aaaagataag gaaaagaag ttgcaacaca acaacaacca 180
 gacaatcaaa ccgttgaaca accccaatca caagagcaat cggttcaaca accgcaaca 240
 cagataccac aaaatagtgt tctcagcaa aatgtccaag ttcaacaaaa caaaaagcaa 300
 aaagttgatt taaataatat gcctcccact gatttttcta cagagggtat gtctgagcag 360
 gctcaaaaac aattgaaga gctttcaatg caaaaagact atcatggtct gtcacaaaga 420
 gaatacaatg atagagtttc tgaattata aataatgata attga 465

<210> SEQ ID NO 21
 <211> LENGTH: 555
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 21

atggtaaaag gatgcgcggtg ttgccttatt tcttttatta tattaattat cttattatca 60
 gcctgttcaa tgatgttttag taataatgac aattccacta gtaatcaatc atcaaaaacg 120
 caattaactc aaaaagacga agataaaagt gaaaatatgc ctgaagaaaa atcagaatca 180
 gaaacagata aggatttaca atcaaccgaa gaagtaccgg caaatgaaaa tactgaaat 240
 aatcaacatg aattgatga aataacaaca acagatcaat cagatgatga aattaacaca 300
 ccaaacgttg cagaagaaga atcacaagat gacttgaaag atgatttaa agaaaagcaa 360
 caaccaagtg accatcatca atccacgcaa cctaagactt caccatcaac tgaacaaaac 420
 aagcaacaat catttgctaa ttgtaagcaa cttagacaag tatatccgaa tgggtgctact 480
 gccgatcatc cagcatatcg accacattta gatagagata aagataaacg tgcattgtgaa 540
 cctgataaat attaa 555

<210> SEQ ID NO 22
 <211> LENGTH: 390
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 22

atgaagaat taatcatcag cattatggcg atcatgctat ttttaacagg ttgtggtaaa 60
 agccaagaga aagccactct ggaaaaggat atcgataatt tacaaaaaga aaataaagaa 120
 ttaaagata aaaaagaaaa gcttcaaca gaaaagaaa aattagcaga taagcaaaaa 180
 gaccttgaaa aagaagtga agatttaaaa ccttcaaaag aagataacaa ggacgataaa 240
 aaagacgaag acaaaaataa agacaagat aaagaggcat cacaagataa gcaatcaaaa 300

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gatcaaaacta agtcatcggga taaagataat cacaaaaagc ctacatcaac agataaagat 360
caaaaagcta atgacaaaaca ccaatcataa 390

<210> SEQ ID NO 23
<211> LENGTH: 2982
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 23

atgaagaacg catttaaatt atttaaaatg gatctgaaga aagtagctaa gacgccagct 60
gtgtggatta tcttagcagg cttagctatt ttgccatcgt tctacgcttg gtttaactta 120
tgggcaatgt gggatccata tggcaacacg ggacacatca aggtcgcagt cgttaatgaa 180
gataaaggcg acacaatcag agggaaaaaa gttaatgtcg gtaatacgat ggtaacaca 240
ctcaagaaaa ataaaagtgtt tgattggcag tttgtaagta gagagaaagc tgatcatgag 300
ataaaaatgg gtaaatatgt tgcaggtatt tacatcccat ctaagtttac acatgaaatt 360
accgggacac tacgtaagca gcctcaaaaa gcagatgtag aatttaaggt gaatcagaag 420
attaacgctg ttgcgtctaa gctaacagat actggttcgt cagttgtcgt tgaaaaagcg 480
aatgaacaat ttaataaaac agtaactcga gcattattag aagaagctaa caaagcaggt 540
ttaactattg aagaaaatgt gccgacaatt aataagataa aaaatgcggt atattcggca 600
gataaagcct tacctaagat taatgacttt gcgaataaaa ttgtatattt gaataaccac 660
caagcggatt tagataaata tgcgaatgat tttagaaaac taggaaatta taaaggtgat 720
atthtagatg ctcagaaaaa attaaacgaa gtcaatgggtg ctattccgca acttaatgaa 780
aaggctaagt tgatattagc tttaaataat tatatgccga aaattgaaaa agcgttaaat 840
tttgacgctg atgacgtgcc agcgcagttc cctaaaaatta atcaaggact taacattgcg 900
agtcaaggta ttgatcaagc taatggacag ttaaatgatg ccaaaggctt cgtcacacaa 960
gttagaagta gagtcggtga ttatcaagaa gcaattcgac gcgcgcaaga tttgaatcga 1020
agaaaccagc aacagattcc tcaaaatagc gggcgcaaca acgaaacatc aaatagtgca 1080
cctgcagctg gtaatgggtg aacatcaacg ccaccaagtg caccaaattg caatactaca 1140
ccaaataata atgttacgca aaataccgca ccaaatagta ataatgcacc tgtatcgact 1200
acaccacaaa gtacaagcgg gaaaaaagat ggtcaaagtt ttgcagatat aacaacaaca 1260
caagtcagca cagctaacga gaacacacaa aatattacag ataagatgt taaatcaatg 1320
gaagcggcat taacgggctc tttattatca ttatcaaata atttagatag ccaagcgaaa 1380
gccgcacaaa aagatagtca ggcattacgt aatatttcgt atggcatttt agcatcggac 1440
aagccatctg atthtagaga gtcttttagat aatgttaagt ccggtttaga atacacaact 1500
caatataatc aacaatttat cgatacatta aaagagattg agaagaatga aaatgttgat 1560
ttatcaaaag aaattgataa ggtaaagaca gctaataatc gaattaatga atcattaagg 1620
ttagttaatc aattaagtaa tgcattaaag aatggtagtt caggaactgc tgaagctact 1680
aaattactag atcaactgtc aaaactagat tcatcattat catcatttag agattatggt 1740
aaaaaagatc ttaacagctc tttagtatca atatcacacac gtattatgga tgaattgaac 1800
aaagggcaaa cggcattgtc taatgttcag tctaagctaa atacaattga tcaagtcac 1860
aacagtggtc aatctattht aaaaaatggt aaaacacgta tcgatcgttt acaaacagta 1920
ttaccaagta ttgaacaaca atacattagt gctattaaaa atgctcaagc aaacttccc 1980
aaagtgaaaa gtgatgtagc gaaagcagct aactttgtac gtaacgattt accacagttg 2040

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gagcaacggt taaccaatgc gactgcaagt gtgaataaaa atttaccac gttattaat 2100
ggttatgac aagcggtagg attactaaat aaaaatcagc cacaagcgaa aaaggctta 2160
tcagatttag ctgattttgc aaaaaataa ttgccagatg ttgaaaaaga tctgaaaaaa 2220
gogaataaga tttcaagaa gttagacaaa gacgatgcag tcgataaatt aatcgacaca 2280
cttaagaatg atttgaaaa gcaagcgggt attattgcaa atcctattaa taagaagact 2340
gttgatgttt tcccagtaa ggattatgga tcagggatga caccattcta tactgcatta 2400
tcggtatggg tagggcact cttaatggta agcctattaa ctgttgataa taaacataag 2460
agcttagagc cagtgttaac gacacgaca gtattcctag gtaaagcagg attctttata 2520
atgcttggtg tggtgcaagc actcattgta tcggttggag atttgtaat cctaaaagca 2580
ggagttgagt cacctgtatt atcgtactt ataacgattt tctgttcgat tttttcaac 2640
tcaatcgtat atacgtgogt atcattactt ggtaaccag gtaaagccat tgcaatcgta 2700
ttgcttggtat tacaattgca aggtggtgga ggtacattcc caattcaaac gacaccacaa 2760
tttttccaaa acatttcgcc atacttacca tttacgtatg caattgatc attacgtgaa 2820
acagtaggog gtattgttcc gaaaatccta attacaaaat taattatatt aacgttattt 2880
ggcataggat tcttcgttgt aggtttaatt ttaaacctg taacagatcc attgatgaag 2940
cgcgatctg aaaaagtga ccaagtaac gttacagaat aa 2982

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<210> SEQ ID NO 24

<211> LENGTH: 6201

<212> TYPE: DNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 24

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atgaatgaaa aagtagaagg catgaccttg gagctgaaat tagaccattt aggtgtccaa 60
gaaggcatga aaggtttaa ggcacaatta ggtgttgta atagtgaaat gaaagctaat 120
ctgtcagcat ttgataagtc tgaaaaatca atggaaaaat atcaggcgag aattaagggg 180
ttaaatagata ggcttaaaagt tcaaaaaaag atgtattctc aagtagaaga tgagcttaaa 240
caagttaacg ctaattacca aaaagctaaa tccagtgtaa aagatgttga gaaagcatat 300
ttaaagttag tagaagccaa taaaaaagaa aaattagctc ttgataaatc taagaagcc 360
ttaaatacat cgaatacaga acttaaaaaa gctgaaaatc aatataaacg tacaatacaa 420
cgtaaaacag atgcgtatca aaaacttaaa cagttgagag atgcagaaca aaagcttaag 480
aatagtaacc aagctactac tgcacaacta aaaagagcaa gtgacgcagt acagaagcag 540
tccgctaagc ataagcact tgttgaacaa tataaacaag aaggcaatca agttcaaaaa 600
ctaaaagtgc aaaatgacaa tctttcaaaa tcaaatgata aaattgaaag ttcttacgct 660
aaaactaata ctaaattaa gcaaacagaa aaagaattta atgatttaaa caatactatt 720
aagaatcata gcgctaagt cgcaaaagct gaaacagctg ttaataaaga aaaagctgct 780
ttaaataaatt tggagcgttc aatagataaa gcttcatccg aaatgaagac ttttaacaaa 840
gaacaaatga tagctcaag tcatttcggt aaacttgcaa gtcaagcggg tgtcatgtca 900
aagaaattta gttctattgg agacaaaatg acttcctcgg gacgtacaat gacgatgggc 960
gtatctacac caattacttt agggttaggt gcagcattaa aaacaagtgc agactttgaa 1020
ggccaaatgt ctcgagttgg agcgattgag caagcaagca gtaaagactt gaaaagcatg 1080
tctaatacaag cagttgactt aggagctaaa accagtaaaa gtgctaacga agttgctaaa 1140

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| | |
|--|------|
| ggtatggaag aattggcagc tttaggcttt aatgcctaac aaacaatgga ggctatgcca | 1200 |
| ggtgttatca gtgcagcaga agcaagtggg gcagaaatgg ctacaactgc aactgtaatg | 1260 |
| gcttcagcga ttaactcttt cggtttataa gcatctgatg caaatcatgt tgctgattta | 1320 |
| cttgcgagat cagcaaatga tagtgctgca gatattcagt acatgggaga tgcattgaag | 1380 |
| tatgctggta ctctctgaaa agcattagga gtttcaatag aggacacttc cgcagcaatt | 1440 |
| gaagttttat ctaactcagg tttagagggt tctcaagcag gtactgcctt aagagcttca | 1500 |
| tttatcaggc tagctaattc aagtaaaaat acagctaagg aaatgaaaaa attaggtatt | 1560 |
| catttgctcg atgctaaagg tcaatttggg ggcattgggt aattgattag acagttccaa | 1620 |
| gataaatgca aaggcatgac gagagaacaa aaactagcta cagtggctac aatagttggt | 1680 |
| actgaagcag caagtggatt tttagccttg attgaagcgg gaccagataa aattaatagc | 1740 |
| tatagtaaat ccttaaagaa ttccaatggc gaaagtaaaa aagcagcaga tttgatgaaa | 1800 |
| gataatctca aaggcgtctt ggaacaatta ggtggcgtt ttgaatcatt agcaatcgaa | 1860 |
| gtcggtaaa atttaacgct tatgattaga gcaggagcgg aaggtttaa aaaattagtt | 1920 |
| gatggattta cacatctccc tggttgggtt agaaaagctt cagttaggatt agcacttttt | 1980 |
| ggtgcatcta ttggcctgct tgttcttggg ggtggcttat taatacgtgc agttggaagt | 2040 |
| gctgctaaag gctatgcatc attaaataga cgcattgctg aaaatacaat actgtcta | 2100 |
| accaattcaa aagcaatgaa atcttttagg cttcaaacct tatttcttgg ttctacaaca | 2160 |
| ggaaaaacgt caaaaaggctt taaaggatta gccggagcta tggttgttaa tttaaaacct | 2220 |
| ataaatgttt tgaaaaattc tgcaaaagca gcaattttac cgttcaaac tttgaaaaac | 2280 |
| ggttttaggat tagccgcaaa atccttattt gcagtaagtg gaggcgcaag atttgctggt | 2340 |
| gtagccttaa agtttttaac aggacctata ggtgctacaa taactgctat tacaattgca | 2400 |
| tataaagttt ttaaaaccgc atatgatcgt gtggaatggt tcagaaacgg tattaacggt | 2460 |
| ttaggagaaa ctataaagtt ttttgggtgc aaaattattg gcggtgctgt taggaagcta | 2520 |
| ggagagttta aaaattatct tggaaatata ggcaaaagct tcaagaaaa gttttcaaa | 2580 |
| gatatgaaag atggttataa atctttgagt gacgatgacc ttctgaaagt aggagtcaac | 2640 |
| aagtttaaag gatttatgca aaccatgggc acagcttcta aaaaagcatc tgatactgta | 2700 |
| aaagtgttgg ggaagggtgt ttcaaaagaa acagaaaaag ctttagaaaa atacgtacac | 2760 |
| tattctgaag agaacaacag aatcatggaa aaagtacgtt taaactcggg tcaataaca | 2820 |
| gaagacaaag caaaaaaact tttgaaaatt gaagcggatt tatctaataa ccttatagct | 2880 |
| gaaatagaaa aaagaaataa aaaggaactc gaaaaaactc aagaacttat tgataagtat | 2940 |
| agtcggttgc atgaacaaga aaagcaaac attttaacta gaactaaaga aaaaaatgac | 3000 |
| ttgcgaatta aaaaagagca agaactcaat cagaaaatca aagaattgaa agaaaaagct | 3060 |
| tttaagtgat gtcagatttc agaaaatgaa agaaaaagaa ttgaaaagct tgaaaatcaa | 3120 |
| agacgtgaca tcaactgtaa agaattgagt aagactgaaa aagagcaaga gcgtatttta | 3180 |
| gtaagaatgc aaagaaacag aaattcttat tcaatagacg aagcagacaa agcaattaaa | 3240 |
| gaagcagaaa aagcaagaaa agcaaaaaaa aaagaagtgg acaagcaata tgaagatgat | 3300 |
| gtcattgcta taaaaataa cgtcaaacctt tctaagtctg aaaaagataa attattagct | 3360 |
| attgctgac aaagacataa ggaatgaagta agaaaggcaa aatctaaaa agatgctgta | 3420 |
| gtagacgttg ttaaaaagca aaataaagat attgataaag agatggattt atccagtggt | 3480 |
| cgtgtatata aaaactga aaatgggtg aatggcctta aaagtgggtg gtctaacttc | 3540 |

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| | | | | | | |
|--------------|-------------|------------|-------------|-------------|-------------|------|
| agagaagacc | aaaagaagaa | aagtgataag | tacgctaaag | aacaagaaga | aacagctcgt | 3600 |
| agaaacagag | aaaatataaa | gaaatggttt | ggaaatgctt | gggacggcgt | aaaaagtaaa | 3660 |
| actggcgaag | cctttagtaa | aatgggcaga | aatgctaata | atthttggcgg | cgaaatgaaa | 3720 |
| aaaatgtgga | gtggaatcaa | aggaattcca | agcaaatata | gttcaggttg | gagctcagcc | 3780 |
| aaaagtcttg | taggatata | cactaaggct | atagctaata | gtactggtaa | atggtttga | 3840 |
| aaagcttggc | aatctgttaa | atcgactaca | ggaagtattt | acaatcaaac | taagcaaaa | 3900 |
| tattcagatg | cctcagataa | agcttggcgg | cattcaaaa | ctatthggaa | agggacatca | 3960 |
| aaatggttta | gcaatgcata | taaaagtga | aagggtggc | taacggatat | ggctaataaa | 4020 |
| tcgctcga | aatgggataa | tatttctagt | acagcatggt | cgaaatgcaa | atcggthttg | 4080 |
| aaaggaacat | cgaaatggtt | tagtaactca | tacaaatctt | taaaaggttg | gactggagat | 4140 |
| atgtattcaa | gagcccacga | tcgthttgat | gcaatthcaa | gttcggcatg | gtctaacgct | 4200 |
| aatcagtat | ttaatggtht | tagaaaatgg | ctatcaagaa | catatgaatg | gatttagatg | 4260 |
| attgtaaa | acatgggaag | agctgcggct | gatttaggta | aaaatgttg | taataaagct | 4320 |
| attgctggth | tgaatagcat | gattgctgg | attaataaaa | tatctaaagc | cattactgat | 4380 |
| aaaaatctca | tcaagccaat | acctacattg | tctactggta | ctthtagcag | aaaggtgta | 4440 |
| gctaccgata | atctgggagc | attaacgcaa | cgcacatttg | ctgtattaaa | tgatagaggt | 4500 |
| tctggaaacg | cccagcggg | tggagthcaa | gaagtaattc | acagggctga | cggaacattc | 4560 |
| catgcacccc | aagacgaga | tgtgthttg | ccactaggag | ttggagatag | tgtaataaat | 4620 |
| gccaatgaca | ctctgaagtt | acagcggatg | ggtgthttg | caaaattcca | tggtggtacg | 4680 |
| aaaaagaaaa | aatggatgga | acaagttact | gaaaatcttg | gtaaaaaagc | aggggacttc | 4740 |
| ggttctaag | ctaaaaacac | agctcataat | atcaaaaaag | gtgcagaaga | aatggtgaa | 4800 |
| gcccagggcg | ataaaatcaa | agatggtgca | tcttgthtag | gcgataaaat | cggcgatgtg | 4860 |
| tgggattatg | tacaacatcc | agggaaacta | gtaataaag | taatgctcag | thtaaatatt | 4920 |
| aatthttgag | gctgagctaa | cgtcacagta | aaaatthgta | aaggctcgta | ctcattgctc | 4980 |
| aaaaagaaat | tagtagacaa | agtaaaatcg | tggthtgaag | atthttgthg | tgagggcagat | 5040 |
| ggaagctatc | tatthgacca | tccaatthtg | caaagthttg | ggagctacac | aggtggactt | 5100 |
| aactthaatg | gctgctgca | ctatgthtgc | gactthcaaa | tgctactgg | aacgaacatt | 5160 |
| tatgctgthta | aagcggtht | agctgataaa | gtatggactg | attacgthtg | cggtaattct | 5220 |
| atacaaatata | agaccgthg | taacgaatgg | aactgthata | tgcatthtgc | taagcaatta | 5280 |
| gcaagacaag | gccaacgtht | taaagctgth | caactgthtag | ggaaatcag | tgctacaggt | 5340 |
| aatthctgthta | gagagcaca | cttacattht | caatthgthg | aagggctcga | tccagggtht | 5400 |
| gatacagctata | aagatccaga | aaaatgthtg | aagthcactta | aagthagthg | cgttcgaagt | 5460 |
| ggtthcagthg | thtaataagc | tgcatctgct | tgggcagggc | atatacgtc | tgcaaaaa | 5520 |
| cgaatggthg | ttaatgtht | tctggthgth | gthagaaata | thattagctt | gattcaaac | 5580 |
| gaaatcagthg | gaaatgcaag | tataactcaa | tctagthgct | thtagacat | caacgththt | 5640 |
| cagggcaatc | cagcaaaag | atgctthcaa | tatactccac | aaacatthtag | acattatgct | 5700 |
| gthtaggthg | acaacaatata | atatagthg | tacgactcag | thattagctt | ctthtaaac | 5760 |
| agctatthg | gctcacagth | taaccaaga | gthgthttg | ctccaagthg | tccaagaaga | 5820 |
| tatgcgaatg | gtgthttgat | tacaaagcat | caactgctg | aagthgthg | agthagataaa | 5880 |

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caggagatgg ttatcccttt aactagacgt aaacgagcaa ttcaattaac tgaacaggtt 5940
atgcgcatca tcggtatgga tggcaagcca aataacatca ctgtaaataa tgatacttca 6000
acagttgaaa aattggtgaa acaaattggt atgttaagtg ataaaggaaa taaattaaca 6060
gatgcattga ttcaactgt ttcttctcag gataataact taggttctaa tgatgcaatt 6120
agaggtttag aaaaaatatt gtcaaaacaa agtgggcata gagcaaatgc aaataattat 6180
atgggaggtt tgactaatta a 6201

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<210> SEQ ID NO 25
<211> LENGTH: 1830
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

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<400> SEQUENCE: 25

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atgaaaaagc aaataatttc gctaggcgca ttagcagttg catctagctt atttcatggt 60
gataacaaag cagatgcatg agtaactaaa gattatagta aagaatcaag agtgaatgag 120
aacagtaaat acgatacacc aattccagat tggatcttag gtagtatttt aaacagatta 180
ggggatcaaa tatactacgc taaggaatta actaataaat acgaatatgg tgagaaagag 240
tataagcaag cgatagataa attgatgact agagttttgg gagaagatca ttatctatta 300
gaaaaaaga aagcacaata tgaagcatac aaaaaatggt ttgaaaaaca taaaagttaa 360
aatccacatt ctagtttaaa aaagattaaa ttgacgatt ttgatttata tagattaacg 420
aagaagaat acaatgagtt acatcaatca ttaaagaag ctgttgatga gtttaatagt 480
gaagtgaaaa atattcaatc taacaaaag gatttattac cttatgatga agcaactgaa 540
aatcgagtaa caaatggaat atatgatttt gtttgcgaga ttgacacatt atacgcagca 600
tattttaatc atagccaata tggtcataat gctaagaat taagagcaaa gctagatata 660
attcttgggt atgctaaaga tcctgttaga attacgaatg aaagaataag aaaagaatg 720
atggatgatt taaattctat tattgatgat ttctttatgg atacaaacat gaatagacca 780
ttaaacataa ctaaatttaa tccgaatatt catgactata ctaataagcc tgaaaataga 840
gataacttgc ataaattagt caaagaaca agagaagcaa tcgcaaacgc tgacgaatct 900
tggaaaacaa gaaccgcaa aaattacggt gaatctgaaa caaaatctcc tgttgtaaaa 960
gaagagaaga aagttgaaga acctcaatta cctaagttg gaaaccagca agaggataaa 1020
attacagttg gtacaactga agaagcacca ttaccaattg cgcaaccact agttaaatt 1080
ccacagggca caattcaagg tgaattgta aaaggtccgg aatatctaac gatggaaaat 1140
aaaaacgttac aagtgaaat cgttcaaggt ccagatttcc caacaatgga acaaaaacaga 1200
ccatctttaa gcgataatta tactcaaccg acgacaccga accctatttt aaaaggtatt 1260
gaaggaaact caactaaact tgaataaaaa ccacaaggtg ctgaatcaac gttaaaagggt 1320
actcaaggag aatcaagtga tattgaagtt aaacctcaag caactgaaac aacagaagca 1380
tcacattatc cagcgagacc tcaatttaac aaaacaccta agtatgtgaa atatagagat 1440
gctggtacag gtatccgtga atacaacgat ggaacatttg gatatgaagc gagaccaaga 1500
ttcaacaagc caagcgaac aaatgcatac aacgtaacga caaatcaaga tggcacagta 1560
tcatatggcg ctcgcccgcg acaaaaacaag ccaagcgaac caaacgcata taacgtaaca 1620
acacatgcaa acggccaagt atcatacggg gctcgtccga cacaaaaaca gccaaagcga 1680
acgaacgcat ataacgtaac aacacatgca aacggtcaag tgtcatacgg agctcgccca 1740
acacaaaaa agccaagtaa aacaaatgca tacaatgtaa caacacatgc agatggtact 1800

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gcgacatatg gtctagagt aacaaaataa 1830

<210> SEQ ID NO 26
 <211> LENGTH: 435
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 26

atgaaaaaag taatcggact gctactagta agtacattag ctttaacagc ttgtggtgaa 60
 aaagaaaaac caaaaaaga agaaaataaa aagtcacaaa cacaaaaaca caaagatagc 120
 aaacaaaaaa cgcaacaaga aaaaatgaaa aaagttgaag ataaaaatcc acctaataat 180
 agcatacaaa ataattcaaa caatcaaaac caatcacaaa acaatcaact taataataat 240
 tcagatccat ctaataatac tctcgcaaat ataaataaaa acgattcaca aaataactaat 300
 ttaaagtatg agtatgtcgt ttcgcctggc tggactaaag atgaacaggc taaagctttt 360
 gaagagtaca aaaagggaaa agaagacgaa gcaagagctg gtgctagcgc agtaccaggga 420
 gccaatatta actaa 435

<210> SEQ ID NO 27
 <211> LENGTH: 3774
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 27

atggcgaaaa aatttaatta caaactacca tcaatggttg cattaacgct tntaggttca 60
 gcagtcactg cacatcaagt tcaagcagct gagacgacac aagatcaaac tactaataaa 120
 aatgttttag atagtaataa agttaagca actactgaac aagcaaaagc tgaggtaaaa 180
 aatccaacgc aaaacatttc tggcactcaa gtatatcaag accctgctat tgtccaacca 240
 aaagcagcga ataaaacagg caatgctcaa gtaaatcaaa aggttgatac tacacaagta 300
 aatggtgaca ctcgtgcgac tcaatcaact acatcaata atgcgaaacc tgttacaag 360
 tcaacaaaaca caacagcacc taaaacgaac aataatgta caagtgtgg atatagtta 420
 gttgatgatg aagatgataa ttcagaaaat caaatataac cagaattaat taaatcagct 480
 gctaaacctg ctgctcttga aacgcaatat aaagccgcag caccaaaagc aacacctggt 540
 gcacctaaag ctaaaactga agtacacca aaagtaacta cttttagtgc ttcagcacia 600
 ccaagatcag ccgctgcagc acctaaaacg agtttgcaa aatataaacc gcaagtaaac 660
 tcatcaatta atgattacat tcgtaaaaat aatttaaaag cacctaagat agaggaagat 720
 tatacatctt acttccctaa atacgcatac cgtaacggtg taggtcgtcc tgaaggtatc 780
 gttgttcag atacagctaa tgategttcg acgataaatg gcgaaattag ttatatgaaa 840
 aacaactatc aaaacgcatt cgtacatgca tttgttgatg gggatcgtat aatcgaaaca 900
 gcaccaacgg attacttatac ttgggggtgc ggtgcagtcg gtaaccctag attcatcaat 960
 gttgaaatcg tgcacacaca cgattatgct tcatttgcac gttcaatgaa taactatgct 1020
 gactatgcag ctacacaatt acaatattat ggtttaaaac ctgatagtcg tgaatatgat 1080
 ggaaatggta cagtatggac tcaactagct gtaagtaaat atttaggtgg tacggaccat 1140
 gccgatccac atggatattt aagaagtcac aattatagtt atgatcaact atagactta 1200
 attaatgaaa aatatttaac aaaaatgggt aaagtggcgc catgggttac gcaatctaca 1260
 actaccctca ctacaccatc aaaaccatca acaccgtgca aaccatcaac accatcaact 1320

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| | |
|---|------|
| ggtaaattaa cagttgctgc taataatggt gtcgcacaaa tcaaacctac aaatagtgg | 1380 |
| ttataatacta ctgtttacga caaaactggt aaagcaacta atgaagtcca aaaaacattt | 1440 |
| gctgtatcta aaacagctac attaggaat caaaaattct atcttggtca agattacaat | 1500 |
| tctggaata aatttggttg ggtaaagaa ggcgatgtgg tttacaacac agctaaatca | 1560 |
| cctgtaaag taaatcaatc atattcaatc aaacctggtc cgaaacttta tacagtacct | 1620 |
| tggggtacat ctaaacaaagt tctggtgtagc gtgtctggtt ctggaaacca aacatttaag | 1680 |
| gcttcaaagc aacaacaaat tgataaatca atttatttat atggctctgt gaatggtaaa | 1740 |
| tctggttggg taagtaaagc atatttagtt gatactgcta aacctacgcc tacaccaaca | 1800 |
| cctaagccat caacacctac aacaaataat aaattaacag tttcatcatt aaacggtggt | 1860 |
| gctcaaatta atgctaaaa caatggctta ttcactacag tttatgacaa aactggtaag | 1920 |
| ccaacgaaag aagttcaaaa aacatttgct gtaacaaaag aagcaagtct aggtggaac | 1980 |
| aaattctact tagttaaaga ttacaatagt ccaactttaa ttggttgggt taaacaagg | 2040 |
| gacgttattt ataacaatgc aaaatcacct gtaaatgtaa tgcaactta tacagtaaaa | 2100 |
| ccaggcacta aattatattc agtaccttgg ggtacttata aacaagaagc tggtagcgtta | 2160 |
| tctggtacag gtaaccaaac ttttaagcg actaagcaac aacaaattga taaatctatc | 2220 |
| tatttatatg gaactgtaaa tggtaaatct ggttgataa gtaaagcata ttagctgta | 2280 |
| cctgctgcac ctaaaaaagc tgtagcacia ccaaaaactg ctgtaaaagc ttatgctggt | 2340 |
| actaaacctc aaacgactca aacagttagc aaaattgctc aagttaaac aaacaacact | 2400 |
| ggtattcgtg cttctgttta tgaaaaaca gcgaaaaacg gtgcaaaata tgcggatcgt | 2460 |
| acattctatg taacaaaaga acgtgcacat ggtaatgaaa catacgtatt attaaataat | 2520 |
| acaagtcata atattccatt aggttggttc aatgtaaaag acttaaatgt tcaaaactta | 2580 |
| ggcaagaag ttaaacgac tcaaaaatat actgttaaca gatcaataa cggcttatca | 2640 |
| atggttcctt ggggtactaa aaaccaagtc attttaacag gcaataacat tgctcaagg | 2700 |
| acatttaatg caacgaaaca agtatctgta ggcaagatg tttatttata cggtagctatt | 2760 |
| aataaccgca ctggttgggt aaattcaaaa gatttaactg caccaactgc tgttaaacca | 2820 |
| actacatcag ctgccaaaga ttataactac acttatgtaa ttaaaaatgg taatggttat | 2880 |
| tactatgtaa caccaaatc tgatacagct aaatactcat taaaagcatt taatgaacaa | 2940 |
| ccattcgcag ttgtaaaaga acaagtcatt aatggacaaa cttggtacta tggtaaatta | 3000 |
| tctaaccgta aattagcatg gattaaatca actgatttag ctaaagaatt aattaagtat | 3060 |
| aatcaaatag gtatgacatt aaaccaagtt gctcaaatc aagctggttt acaatataaa | 3120 |
| ccacaagtac aacgtgtacc aggtaagtgg acagatgcta actttaatga tggtaagcat | 3180 |
| gcaatggata cgaagcgttt agctcaagat ccagcattaa aatatcaatt cttacgctta | 3240 |
| gaccaaccac aaaatatttc tattgataaa attaatcaat tcttaaaagg taaaggtgta | 3300 |
| ttagaaaacc aaggtgctgc atttaacaaa gctgctcaaa tgtatggcat taatgaagtt | 3360 |
| tatcttatct cacatgccct attagaacaa ggtaacggta cttctcaatt agcaaaagg | 3420 |
| gcagatgtag tgaacaacaa agttgtaact aactctaaca cgaaatacca taacgtattt | 3480 |
| ggtattgctg catatgataa cgatccttta cgtgaaggta ttaaatatgc taaacaagct | 3540 |
| ggttgggaca cagtatcaaa agcaatcgtt ggtggtgcta aatcctcgg caactcatat | 3600 |
| gttaaagctg gtcaaaatc gctttacaaa atgagatgga atcctgcaca tccaggaaca | 3660 |
| accaaatatg ctacagatgt agattgggct aacatcaatg ctaaaatcat caaaggctac | 3720 |

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 tatgataaaa ttggcgaagt cggcaaatc ttcgacatcc cacaatataa ataa 3774

<210> SEQ ID NO 28
 <211> LENGTH: 1461
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 28

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 catcaagacc atacggaaga tgttgaaaaa gaccaatcag aattagaaca tcaggatata 120
 atagagaata cggagcaaca gtttccgcca agaaatgccc aaagaagaaa aagacgccgt 180
 gatttagcaa cgaatcataa taaacaagtt cacaatgaat cacaaacatc tgaagacaat 240
 gttcaaaatg aggctggcac aatagatgat cgtcaagtcg aatcatcaca cagtactgaa 300
 agtcaagaac cttagcatca agacagtaca cctcaacatg aagagggata ttataataag 360
 aatgcttttg caatggataa atcacatcca gaaccaatcg aagacaatga taaacacgag 420
 actattaag aagcagaaaa taactctgag cattcaacag tttctgataa gagtgaagct 480
 gaacaatctc agcaacctaa accatatttt gcaacaggtg ctaaccaagc aaatacatca 540
 aaagataaac atgatgatgt aactgttaag caagacaaag atgaatctaa agatcatcat 600
 agtggtaaaa aaggcgcagc aattgggtgct ggaacagcgg gtgttgccagg tgcagctggt 660
 gcaatgggtg tttctaaagc taagaacat tcaaatgacg ctcaaaacaa aagtaattct 720
 ggcaagtgta ataactcgac tgaggataaa gcgtctgaag acaagtcaaa agaacatcat 780
 aatggtaaaa aagggtgcagc aatcggtgct ggaacagcag gtttggctgg aggcgcagca 840
 agtaatagtg cttctgcccg tcaaaaacca catgcctcta ataatgcaag tcaaaaacaat 900
 gatgaacatg accatcatga cagagataaa gaacgtaaaa aaggtggcat ggccaaagta 960
 ttgttaccat taattgcagc tgtactaatt atcgggtgcat tagcgatatt tggaggcatg 1020
 gcattaaaca atcataataa tggtaaaaaa gaaaataaaa tcgcgaatac aaataaaaat 1080
 aatgctgatg aaagtaaaga taaagacaca tctaagacg cttctaaaga taaatcaaaa 1140
 tctacagaca gtgataaatc aaaagatgat caagacaaag cgactaaaga tgaatctgat 1200
 aatgatcaaa acaacgctaa tcaagcgac aatcaagcac aaaataatca aaatcaacaa 1260
 caagctaadc aaaatcaaca acagcaacaa caacgtcaag gtggtggcca aagacataca 1320
 gtgaatggtc aagaaaactt ataccgtatc gcaattcaat actacggttc aggttcaccg 1380
 gaaaatgttg aaaaaattag acgtgccaat ggtttaagtg gtaacaatat tagaaacggt 1440
 caacaaatcg ttattccata a 1461

<210> SEQ ID NO 29
 <211> LENGTH: 3825
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 29

atgagctggt ttgataaatt attcggcgaa gataatgatt caaatgatga cttgattcat 60
 agaaagaaaa aaagacgtca agaatacaaa aatatagata acgatcatga ctactactg 120
 cctcaaaata atgatattha tagtcgtccg aggggaaaaa tccgttttcc tatgagcgtg 180
 gcttatgaaa atgaaaatgt tgaacaatct gcagatacta tttcagatga aaaagaacaa 240
 taccatcgag actatcgcaa acaaagccac gattctcgtt cacaaaaacg acatcgccgt 300

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| | |
|--|------|
| agaagaaatc aaacaactga agaacaaaat tatagtgaac aacgtgggaa ttctaaaata | 360 |
| tcacagcaaa gtataaaaata taaagatcat tcacattacc atacgaataa gccaggtaca | 420 |
| tatgtttctg caattaatgg tattgagaag gaaacgcaca agtcaaaaac acacaatata | 480 |
| tattctaata atacaaatca tcgtgctaaa gattcaacta cagattatca caaagaaagt | 540 |
| ttcaagactt cagaggtacc gtcagctatt ttggcaca tgaaacctaa aaagttagaa | 600 |
| aatggtcgta tcctgtaag taaatcttca gaaaaagttg agtcagataa acaaaaatat | 660 |
| gataaatatg tagctaagac gcaaacgtct caaaataaac atttagaaca agagaaacaa | 720 |
| aaagatagtg ttgtcaagca aggaactgca tctaatacat ctgatgaaaa tgtatcatca | 780 |
| acaacaaaat caacacctaa ttattcaaaa gttgataata ctatcaaaa tgaaaacatt | 840 |
| tatgcttcac aaattgtga agaaattaga cgtgaacgag aacgtaaagt gcttcaaaag | 900 |
| cgtcgattta aaaaagcgtt gcaacaaaag cgtgaagaac ataaaaacga agagcaagat | 960 |
| gcaatacaac gtgcaattga tgaatgtat gctaacaag cggaacgcta tgttggtgat | 1020 |
| agttcattaa atgatgatag tgaacttaaca gataatagta cagaggctag tcagcttcat | 1080 |
| acaaatgaaa tagaggatga agctgtatca aatgatgaaa ataaaaaacg gtcaatacaa | 1140 |
| aatgaagaca ctgatgacac tcatgtagat gaaagtcct acaattatga ggaagttagt | 1200 |
| ttgaatcaag tatcgacaac aaaacaattg tcagatgatg aagttacggt ttcggatgta | 1260 |
| acgtctcaac gtcaatcagc actgcaacat aacgttgaag taaataatca agatgaacta | 1320 |
| aaaaatcaat ccagattaat tgetgattca gaagaagatg gagcaacgaa tgaagaagaa | 1380 |
| tattcaggaa gtcaaatcga tgatgcagaa ttttatgaat taaatgatac agaagtagat | 1440 |
| gaggatacta cttcaaatag cgaagataat accaatagag acgcgtctga aatgcatgta | 1500 |
| gacgtccta aaacgcaaga gcacgcagta actgaatctc aagttaataa tatcgataaa | 1560 |
| acggttgata atgaaattga attagcgcca cgtcataaaa aagatgacca acaaaactta | 1620 |
| agtgtaact cattgaaaac gaatgatgtg aatgatggtc atgttggtga agattcaagc | 1680 |
| atgaatgaaa tagaaaagca aaacgcagaa attacagaaa atgtgcaaaa cgaagcagct | 1740 |
| gaaagtaaac aaaatgtcga agagaaaact attgaaaacg taaatccaaa gaaacagact | 1800 |
| gaaaaggttt caactttaag taaaagacca tttaatggtg tcatgacgcc atctgataaa | 1860 |
| aagcgtatga tggatcgtaa aaagcattca aaagtcaatg tgctgaatt aaagcctgta | 1920 |
| caaagtaaac aagctgcgag tgaagcaag actgcgactc aaaacacacc atcatcaagt | 1980 |
| actgattcac aagagtcaaa cacgaatgca tataaaacaa ataatatgac atcaaaacat | 2040 |
| gttgagaaca atcaacttat tggatcagca gcaacagaaa atgattatca aaatgcacaa | 2100 |
| caatattcag agcagaaacc ttctgctgat tcaactcaaa cggaaatatt tgaagaaagc | 2160 |
| caagatgata atcaattgga aaatgagcaa gttgatcaat caacttcgtc tcagtttca | 2220 |
| gaagtaagcg acataactga agaaagcgaa gaaacaacac atcaaaacaa tactagtgga | 2280 |
| caacaagata atgatgatca acaaaaagat ttacagcttt cattttcaaa tcaaaatgaa | 2340 |
| gatacagcta atgaaaatag acctcggacg aatcaaccag atgttgcaac aaatcaagct | 2400 |
| gtacaaaact ctaagccgat gattcgtaaa ggcccaata ttaaattgcc aagtgtttca | 2460 |
| ttactagaag aaccacaagt tattgagccg gacgaggact ggattacaga taaaaagaaa | 2520 |
| gaacttaatg acgcattatt ttactttaat gtacctgacg aagtacaaga tgtaactgaa | 2580 |
| ggtccaagtg ttacaagatt tgaattatca gttgaaaaag gtgttaaagt ttcaagaatt | 2640 |
| acggcattac aagatgacat taaatggca ttggcagcga aagatattcg tatagaagcg | 2700 |

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ccaattccag gaactagtcg tgttggatt gaagttccga accaaaatcc aacgacggc 2760
aacttacgtt ctattattga atctccaagt tttaaaaatg ctgaatctaa attaacagtt 2820
gcatgggggt atagaattaa taatgaacca ttacttatgg atattgctaa aacgccacac 2880
gcactaattg caggtgcaac tggatcaggg aatcagttt gtatcaatag tattttgatg 2940
tctttactat ataaaaatca tcttgaggaa ttaagattat tacttattga tccaaaaatg 3000
gttgaattag ctccttataa tggtttgcca catttagttg caccggtaat tacagatgtc 3060
aaagcagcta cacagagttt aaaatgggcc gtagaagaaa tggaaagacg ttataagtta 3120
tttgcacatt accatgtacg taatataaca gcatttaaca aaaaagcacc atatgatgaa 3180
agaatgccaa aattgtcat agtaattgat gagttggctg atttaatgat gatggctccg 3240
caagaagttg agcagtcctat tgctagaatt gctcaaaaag cgagagcatg tggattcat 3300
atgttggtag ctacgcaaag accatctgtc aatgtaatta caggtttaat taaagccaac 3360
ataccaacaa gaattgcatt tatggtatca tcaagtgtag attcaagaac gatattagac 3420
agtgtgggag cagaacgctt gttaggatat ggcatatgt tatactctgg tagcgggatg 3480
aataaaccca ttagagttca aggtacattt gtttctgatg acgaaattga tgatgttgtt 3540
gattttatca aacaacaaag agaaccggac tacctatttg aagaaaaaga attgttgaaa 3600
aaaacacaaa cacaatcaca agatgaatta tttgatgatg tttgtgcatt tatggttaat 3660
gaaggacata tttcaacatc attaatccaa agacatttcc aaattggcta taatagagca 3720
gcaagaatta tcgatcaatt agagcaactc ggttatgttt cgagtgctaa tggttcaaaa 3780
ccaagggatg tttatgttac ggaagcagat ttaaataaag aataa 3825

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<210> SEQ ID NO 30
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

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<400> SEQUENCE: 30
atgtcgaatc aaaattacga ctacaataaa aatgaagatg gaagtaagaa gaaaatgagt 60
acaacagcga aagtagttag cattgacgac gtattgctat tactcggagg attagtattt 120
gcaatttttg catatgtaga tcattcgaat aaagctaaag aacgtatgtt gaacgaacaa 180
aagcaggaac aaaaagaaaa gcgtcaaaaa gaaaatgacg aaaaagagag aaagaaaaag 240
caacaagagg aaaaagagca gaatgagcta gattcacaag caaaccaata tcagcaattg 300
ccacagcaga atcaatatca atatgtgcca cctcagcaac aagcacctac aaagcaacgt 360
cctgctaagg aagagaatga tgataaagca tcaaaggatg agtcgaaaga taaggatgac 420
aaagcatctc aagataaatc agatgataat cagaagaaaa ctgatgataa taaacaacca 480
gctcagccta aaccacagcc gcaacaacca acaccaaacg caaataataa tcaacaaaac 540
aatcaatcaa atcaacaagc gaaaccacaa gcaccacaac aaaaatagcca atcaacaaca 600
aataaacaaa ataatgctaa tgataagtag 630

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```

<210> SEQ ID NO 31
<211> LENGTH: 573
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

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```

<400> SEQUENCE: 31
atgaaattaa aatcattagc agtgttatca atgtcagcgg tgggtgcttac tgcatgtggc 60

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| | |
|---|-----|
| aatgatactc caaaagatga aacaaaatca acagagtcaa atactaatca agacactaat | 120 |
| acaacaaaag atgttattgc attaaaagat gttaaaacaa gcccagaaga tgctgtgaaa | 180 |
| aaagctgaag aaacttacia aggccaaaag ttgaaaggaa tttcatttga aaattcta | 240 |
| ggtgaatggg cttataaagt gacacaacaa aaatctggtg aagagtcaga agtacttgtt | 300 |
| gatgataaaa ataaaaaagt gattaacaaa aagactgaaa aagaagatag agtgaatgaa | 360 |
| aatgataact ttaaatatag cgatgctata gattacaaaa aagccattaa agaaggacia | 420 |
| aaggaatttg atggtgatat taaagaatgg tcacttgaag aagatgatgg taaacttgtt | 480 |
| tacaatatcg atttgaaaaa aggtaataaa aaacaagaag ttactgttga tgctaagaac | 540 |
| ggtaaagtat taaagagtga gcaagatcaa taa | 573 |

<210> SEQ ID NO 32

<211> LENGTH: 3030

<212> TYPE: DNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 32

| | |
|--|------|
| atgaaaaaga aaaattggat ttatgcatta attgtcactt taattattat aattgccata | 60 |
| gttagtatga tattttttgt tcaacaaaaa tatggagatc aatcagaaaa aggatcccaa | 120 |
| agtgtaagta ataaaaataa taaaatacat atcgcaattg ttaacgagga tcaaccaacg | 180 |
| acataatacg gtaaaaagggt tgagctgggt caagcattta ttaaaagggt agcaaatgag | 240 |
| aaaaactata aatttgaaac agtaacaaga aacgttctg agtctggttt gaaaaatggc | 300 |
| ggataccaag tcatgattgt tatccagaa aacttttcaa aattggcaat gcaattagac | 360 |
| gctaaaacac catcgaaat atcactacag tataaacag ctgtaggaca aaaagaagaa | 420 |
| gtagctaaaa acacagaaaa agttgtaagt aatgtactta acgactttaa caaaaacttg | 480 |
| gtcgaattt atttaacaag catcattgat aatttacata atgcacaaaa aaatgttggc | 540 |
| gctattatga cgcgtgaaca tgggtgtaag agtaaatct cgaattactt attaaatcca | 600 |
| attaacgact tcccgaatt atttacagat acgcttgtaa attcgattc tgcaaaaaaa | 660 |
| gatattacaa aatggttcca aacatacaat aaatcattac tgagtgcgaa ttcagataca | 720 |
| ttcagagtga acacagatta taatgtttcg actttaattg aaaaacaaaa ttcattattt | 780 |
| gacgaacaca atacagcgat ggataaaatg ttacaagatt ataatcgca aaaagatagc | 840 |
| gtggaacttg ataactatat caatgcatta aaacagatgg acagccaaat tgatcaacaa | 900 |
| tcaagtatgc aagatacagg taaagaagaa tataaacaaa ctgttaaaga aaacttagat | 960 |
| aaattaagag aatcattca atcacaagag tcaccattt caaaagggtat gattgaagac | 1020 |
| tatcgtaagc aattaacaga atcactccaa gatgagcttg caaacacaa agacttacia | 1080 |
| gatgcgctaa atagcattaa aatgaacaat gctcaattcg ctgaaaactt agagaaacaa | 1140 |
| cttcattgat atattgtcaa agaactgat tcagatacaa catttatcta taacatgtct | 1200 |
| aaacaagact ttatagctgc aggttttaat gaggatgaag ctaataaata cgaagcaatt | 1260 |
| gtcaagaag caaacgtta taaaaacgaa tataatttga aaaaaccgtt agcagaacac | 1320 |
| attaatttaa cagattacga taaccaagtt gcgcaagaca caagtagttt gattaatgat | 1380 |
| ggtgtgaaag tgcaacgtac tgaacgatt aaaagtaatg atattaatca attaaactgtt | 1440 |
| gcaacagatc ctcatthtaa ttttgaagc gacattaaaa ttaatggtaa aaaaatgac | 1500 |
| attaaggatc aaagtgttca actcgataga tctaacaagg aatataaagt tgaagtcaat | 1560 |
| ggcgttgcta aattgaaaaa ggatgctgag aaagatttct taaaagataa aacaatgcat | 1620 |

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ttacaattgt tatttgaca agcaaatcgt caagatgaac caaatgataa gaaagcaacg 1680
agtgttgagg atgtaacatt gaatcataac cttgatggtc gcttatcgaa agatgcatta 1740
agccagcaat tgagtgcatt atctaggttt gatgcgcatt ataaaatgta cacagataca 1800
aaaggcagag aagataaacc attcgacaac aaacgtttaa ttgatatgat ggttgacca 1860
gttatcaatg acatggaaag tttcaaagac gataaagtag ctgtgttaca tcaaattgat 1920
tcaatggaag aaaactcaga caaactgatt gatgacattt taaataacaa aaagaataca 1980
acaaaaaata aagaagatat ttctaagctg attgatcagt tagaaaacgt taaaagact 2040
tttgctgaag agccacaaga accaaaaatt gataaaggca aaaaatgatga atttaatacg 2100
atgtcttcaa atttagataa agaaattagt agaatttctg agaaaagtac gcaattgcta 2160
tcagatacac aagaatcaaa aacaattgca gattcagtta gtggacaatt aaatcaatta 2220
gataataatg tgaataaact acatgcgaca ggtcgcagcat taggcgtaag agcgaatgat 2280
ttgaaccgtc aaatggctaa aaacgataaa gataatgagt tattcgctaa agagttaaa 2340
aaagtattac aaaattctaa agatggcgac agacaaaacc aagcattaaa agcatttatg 2400
agtaatccgg ttcaaaagaa aaacttagaa aatgttttag ctaataatgg taatacagac 2460
gtgatttcac cgacattggt cgtattattg atgtatttac tatcaatgat tacagcatat 2520
attttctata gctatgaacg tgctaaagga caaatgaatt tcatcaaaga tgattatagt 2580
agtaaaaaca atctttggaa taatgcgatt acgtctggtg ttattgggtc aactgggtta 2640
gtagaaggat taattgtcgg ttttaattgca atgaataagt tccatgtatt agctggctat 2700
agagcgaat tcatcttaat ggtgatttta actatgatgg tcttcgtact tattaatacg 2760
tatttactaa gacaggtaaa atctatcggc atgttcttaa tgattgctgc attgggtcta 2820
tactttgtag ctatgaataa tttgaaagcg gctggacaag gtgtgactaa taaaatttca 2880
ccattatctt atatcgataa catgttcttc aattatttaa atgcagagca tccatagggc 2940
ttggcgctag taatattaac agtacttggt attattggct ttgtactgaa catgtttata 3000
aaacacttta agaaagagag attaatctaa 3030

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<210> SEQ ID NO 33
<211> LENGTH: 1191
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

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<400> SEQUENCE: 33

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atgacgcaac acaaaaataa taaaagaaca ttaaaaaata aacacactta tcaaatgaa 60
ccattaccaa accgtaaaga ttttgtgtt agttttataa ctggcgcgct tgttggttca 120
gctttaggct tatattttaa aaataaagtt tatcaaaaag cagatgattt aaaagtcaaa 180
gaacaagaac tgtcgcaaaa gtttgaagaa agaaaaacgc aactgaaga aacggttgcc 240
tttcaaaaag aacgtgttga aggattttta acaaaactta aaaaatgaaca agcggcattg 300
aaggcacaac aagcagcaat aaaagaagaa gcaagtgcaa ataatttaag cgatacatca 360
caagaggcac aagagattca agaagctaaa agagaagcac aaacagaaac ggataaaaagt 420
gcggtctgat caaatgaaga gtcaaaggca tcggcattga aggcacaaca agcagcgata 480
aaagaagaag caagtgcaaa taatttaagt gatacatcac aagaagcaca agcagattcaa 540
gaagtgaaga aagaagcgca agcagaaaca gataaaagtg cagatgtatc aaatgaagaa 600
tcaaaagcat cgacattaaa cgtatcgaaa gaagagtcac aagctgaaag attagcaaac 660

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| | |
|---|------|
| gctgcaaaac agaagcaagc taaattaaca ccaggctcaa aagagagtca attaactgaa | 720 |
| gcgttatttg cagaaaaacc agttgctaaa aatgacttga aagaaattcc tctattagtt | 780 |
| actaaaaaga atgatgtatc agaaacagtt aatacagata ataaagacac tgttaaacaa | 840 |
| aaagaagcta aatttgaaaa tgggtgtatt acacgtaaag ctgatgaaaa aacaccta | 900 |
| aatacagctg ttgacaagaa atcaggtaaa caatctaaaa aaacaacacc ttcaaataaa | 960 |
| cgaaatgcat caaaagcatc gacaaataaa acttcaggtc agaaaaagca acataataag | 1020 |
| aaagcatcac aaggtgcaaa gaaacaaagt agttcaagta actcaacgac aaagactaat | 1080 |
| caaaaaaatt caaaagcaac aaatgctaaa tcatccaatg catcaaaaaa atcaaatgct | 1140 |
| aaagttgaaa aagctaaaag taaaatagag aaacgtacat ttaatgacta a | 1191 |

<210> SEQ ID NO 34

<211> LENGTH: 2310

<212> TYPE: DNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 34

| | |
|---|------|
| gtggatattg gtaaaaaaca tgtaattcct aaaagtcagt accgacgtaa gcgtcgtgaa | 60 |
| ttcttcaca acgaagacag agaagaaaat ttaaatcaac atcaagataa acaaaatata | 120 |
| gataatacaa catcaaaaaa agcagataag caaatacata aagattcaat tgataagcac | 180 |
| gaacgtttta aaaatagttt atcatcgcat ttagaacaga gaaaccgtga tgtgaatgag | 240 |
| aacaaagctg aagaaagtaa aagtaatcag ggtagtaagt cagcatataa caaagatcat | 300 |
| tatttaacag acgatgtatc taaaaaaca aattcattag attcagtaga ccaagatata | 360 |
| gagaaatcaa aatattatga gcaaaatact gaagcgactt tatcaactaa ttcaaccgat | 420 |
| aaagtagaat caactgacat gagaaagcta agttcagata aaaacaaagt tggatcatgaa | 480 |
| gagcaacatg tactttctaa accttcagaa catgataaag agactagaat tgattttgag | 540 |
| tcttcaagaa ctgattcaga cagctcgatg cagacagaga aaataaaaaa agacagttca | 600 |
| gatgaaata aaagtagtaa tctgaaatct gaagtaatat cagacaaatc aaattcagta | 660 |
| ccaatattgt cggaatctga tgatgaagta aataatcaga agccattaac tttgccggaa | 720 |
| gaacagaaat tgaaaaggca gcaaaagtaa aatgagcaaa caaaaactta tacatatggt | 780 |
| gatagcgaac aaaatgacaa gtctaatacat gaaaatgatt taagtcatca tacaccatcg | 840 |
| ataagtgatg ataaagatta cgttatgaga gaagatcata ttgttgacga taatcctgat | 900 |
| aatgatatca atacaccatc attatcaaaa atagatgacg atcgaaaact tgatgaaaaa | 960 |
| attcatgtcg aagataaaca taaacaaaat gcagactcat ctgaaacggg gggatatcaa | 1020 |
| agtcagtcaa gtgcatctca tcgtagcact gaaaaagaa atatggctat taatgaccat | 1080 |
| gataaattaa acggtcaaaa accaaaataca aagacatcgg caaataataa tcaaaaaaag | 1140 |
| gctacatcaa aattgaacaa agggcgcgct acaataataa attatagcgc ctttttgaaa | 1200 |
| aagttttgga tgatgtattg gcctaaatta gttattctaa tgggtattat tattctaatt | 1260 |
| gttattttga atgccatttt taataatgtg acaaaaaatg atcgcgatgaa tgataataat | 1320 |
| gatgcagatg ctcaaaaaata tacgacaacg atgaaaaatg ccaataacgc agttaaatacg | 1380 |
| gtcgttacag ttgaaaatga aacatcaaaa gattcatcat tacctaaaga taaagcatct | 1440 |
| caagacgaag taggatcagg tgtgtatata aaaaaatctg gagatacgtt atatattggt | 1500 |
| acgaatgcac acgttgtcgg tgataaagaa aatcaaaaaa taactttctc gaataataaa | 1560 |
| agtgttgttg gaaaagtgtc tggtaaagat aaatggtcag atttagctgt tgtaaagca | 1620 |

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acttcttcag acagttcagt gaaagagata gctattggag attcaaataa tttagtgtta 1680
ggagagccaa tattagtcgt aggtaatcca cttggtgtag actttaagg cactgtgaca 1740
gaaggtatta tttcaggctc gaacagaaat gttccaattg atttcogata agataataaa 1800
tatgatatgt tgatgaaagc tttccaaatt gatgcatcag taaatccagg taactcgggt 1860
ggtgctgtcg tcaatagaga aggaaaatta attggtgtag ttgcagctaa aattagtatg 1920
ccaaacgttg aaaatatgtc atttgcaata cctgttaatg aagtacaaaa gattgtaaaa 1980
gaattagaaa caaaaggtaa aattgactat cccgatgtag gtgttaaaat gaagaatatt 2040
gccagtctaa atagtttga aagacaagca gttaaattgc taggaaaagt taagaacggt 2100
gttgtttag atcaagttga caacaatggt ttagcagatc aatctggtct gaaaaaagg 2160
gatgtaatta ctgaattaga tggcaaacct ttagaagatg atttacgctt taggcagatt 2220
atatttagtc ataaagatga cttgaaatca attacagcga agatttatag agatggtaaa 2280
gaaaaagaaa ttaatattaa actaaaataa 2310

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<210> SEQ ID NO 35
<211> LENGTH: 627
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

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<400> SEQUENCE: 35
atgaaattca aagctatcgt tgcaatcaca ttatcattgt cactattaac cgctgtggt 60
gctaatacaac ataaagaaaa tagtagtaaa tcaaatgaca ctaataaaaa gacgcaacaa 120
actgataaca ctacacagtc aaatacagaa aagcaaatga ctccacaaga agccgaagat 180
atcgttcgaa acgattacaa agcaagaggt gctaacgaaa atcaaacatt aaattataaa 240
acaaatcttg aacgaagtaa tgaacatgaa tattatgttg aacatctagt ccgcatgca 300
gttggcacac cattaanaac ttgcgctatt gttaatcgac acaatggtac gattattaat 360
atthttgatg atatgtcaga aaaagataaa gaagaatttg aagcatttaa aaagagaagc 420
cctaataaca acccaggatg gaatgatcaa gctgaaatgg ataatgagtc ggaagacatt 480
caacatcatg atattgacaa taacaaagcc attcaaatg acttaccaga tcaaaaagtc 540
gatgataaaa acgataaaaa tgctgttaat aaagaagaaa aacacgataa ccgtgaaat 600
aattcagcag aaactaaagt taaataa 627

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<210> SEQ ID NO 36
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

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```

<400> SEQUENCE: 36
atggataaga aaaaagtcac caaatttatg attaatgtat taccaattgt attggtaccg 60
ttaattgttg aacgtaaacg tatcaaacaa catccggacg tacaaaaagt tacagatgct 120
acaagtaaag ttgcttcaaa aacatctgca gcaatcagta acacagcgag tgatgttaaa 180
gaatatgtcg gcgataaaaa acaagatttt gaaaataagc gtgaacttaa aaagtttgct 240
agagaacatg atcctgccta tattgagaaa aaaggcgaaa aattagctaa acaaaatcgt 300
aaagacgctg ataaaatgaa taaaactct caaaaaata tcgaaaagcg tcataaagaa 360
gagcaaaaag ccccgcaaaa gaatgaaata caacgtatta aagatatgaa aaagtcacaa 420
aaatacgaag taaaagcagg cttaacacct aataaattag atgagaaaac tgagaaaaaa 480

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| | |
|---|-----|
| ggcgataaac tagctgaaaa aaatcgcaaa gaaatcgcta aaatgaataa aaagttacaa | 540 |
| aaaaatattg aaaaacgaca caaagaagaa caaaaacgcc aacaagaagc tgataaagca | 600 |
| cgcatcaagt catttaaaaa atataaagat tatgttgcca aaagcgcctc tcaacaaaat | 660 |
| aaagaaaaa atacagaggc ataa | 684 |

<210> SEQ ID NO 37
 <211> LENGTH: 1215
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 37

| | |
|--|------|
| atgtcatatc attggtttaa gaaaatgta ctttcaacaa gtatgttaat ttttaagtagt | 60 |
| agtagtagtt tagggcttgc aacgcacaca gttgaagcaa aggataactt aaatggagaa | 120 |
| aagccaacga ctaatttgaa tcataatgta acttcacat cagtaaaatag tgaatgaat | 180 |
| aataatgaga ctgggacacc tcacgaatca aatcaagctg gtaatgaagg aactggttcg | 240 |
| aatagtcgtg atgctaatac tgattcgaat aatgtgaagc cagactcaaa caacccaaac | 300 |
| ccaagtccag attcaaaacc tgaccctaat aacccaaacc caggtccgaa tccgaagcca | 360 |
| gaccagata agccgaaacc aaatccggaa ccaaagccag acccagataa gccgaaacca | 420 |
| aatccggatc caaaaccaga tccagacaaa ccgaagccaa atccggatcc aaaaccagat | 480 |
| ccaaatccga atccgaatcc aaaaccagac cctaataagc caaatccaaa tccgtctcca | 540 |
| aatcccaatc aacctgggga ttccaatcaa tctggtggct cgaaaaatgg ggggacatgg | 600 |
| aacccaaatg cttcagatgg atctaatac ggtcaatggc aacccaaatg aaatcaagga | 660 |
| aactcacaaa atcctactgg taatgatttt gtatcccaac gatTTTTagc cttggcgaat | 720 |
| ggggcttaca agtataatcc gtatatttta aatcaaatta atcaattggg gaaagaatat | 780 |
| ggtgaggtaa ctgatgaaga tatctacaat atcatccgta aacaaaactt cagcggaaat | 840 |
| gcatatttaa atggattaca acagcaatcg aattacttta gattccaata tttcaatcca | 900 |
| ttgaaatcag aaaggtaacta tcgtaattta gatgaacaag tactcgcatt aattactggc | 960 |
| gaaattggat caatgccaga tttgaaaaag cccgaagata agccggattc aaaacaacgt | 1020 |
| tcatttgagc ctcatgaaaa agatgatttt acagttgtaa aaaaacaaga agataataag | 1080 |
| aaaagtgcgt caactgcata tagtaaaagt tggctagcaa ttgtatgttc tatgatggtg | 1140 |
| gtattttcaa tcatgctatt cttatttgta aagcgaata aaaagaaaa taaaaacgaa | 1200 |
| tcacagcgac gataa | 1215 |

<210> SEQ ID NO 38
 <211> LENGTH: 696
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 38

| | |
|---|-----|
| atgaagaaaa cattactcgc atcatcatta gcagtaggtt taggaatcgt agcaggaaat | 60 |
| gcaggtcacg aagcccaagc aagtgaagcg gacttaata aagcatcttt agcgc aaatg | 120 |
| gcgcaatcaa atgatcaaac attaaatcaa aaaccaatg aagctggcgc ttataattat | 180 |
| acatttgact atgaaggggt tacttatcac tttgaatcag atggtacaca ctttgettg | 240 |
| aattaccatg caacaggtgc taatggagca gacatgagtg cacaagcacc tgcaactaat | 300 |
| aatgttgac catcagctga tcaatctaata caagtacaat cacaagaagt tgaagcacca | 360 |
| caaaatgctc aaactcaaca accacaagca tcaacatcaa acaattcaca agttactgca | 420 |

-continued

```

acaccaactg aatcaaaagc atcagaaggt tcatcagtaa atgtgaatga tcatctaaaa 480
caaatgtctc aacgtgaatc aggtggcaat attcatgctg taaatccaac atcaggtgca 540
gctggtaagt atcaattctt acaatcaact tgggattcag tagcacctgc taaatataaa 600
ggtgtatcac cagcaaatgc tctgaaagt gttcaagatg cgcgagcagt aaaactatat 660
aacactgggtg gcgctggaca ttgggttact gcataa 696

```

```

<210> SEQ ID NO 39
<211> LENGTH: 465
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

```

```

<400> SEQUENCE: 39

```

```

augaaaagau uguuagguuu auuuuuagug agcacguuag uguuaagugc auguggaaa 60
gaugagaauc aggaagaauc uaaaaaagaa guuuuuucaa aagaaaagaa auuugagaag 120
gaaaaggaaa auuuuuucaa aaaagauaag gaaaaagaag uugcaacaca acaacaacca 180
gacaaucaaa ccguugaaca acccccauca caagagcaau cgguucaaca accgcaacaa 240
cagauaccac aaaauagugu uccucagcaa aauguccaag uucaacaaaa caaaaagcaa 300
aaaguugauu uaaauuuuuu gccucccacu gauuuuuucua cagaggguuu gucugagcag 360
gcucaaaaac aaaauagaaga gcuuucaaug caaaaagacu aucauggucu gucacaaaga 420
gaauacaaug auagaguuuu ugaaauuua aauaauugaua auuga 465

```

```

<210> SEQ ID NO 40
<211> LENGTH: 555
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

```

```

<400> SEQUENCE: 40

```

```

auguuuuuag gaugcggcgg uugccuuuuu uuuuuuuuuu uuuuuuuuuu cuuuuuuuuu 60
gccuguucua ugauguuuuu uuuuuuuuuu aaauuauuag aaauuauuag aaauuauuag 120
cauuuuuauu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 180
gaaacagaua aggaauuuua aucaaccgaa gaaguaccgg caaaugaaaa uacugaaaau 240
aaucacaug aaauuagauga auuauuauu aucaaccgaa gaaguaccgg caaaugaaaa uacugaaaau 300
ccaaacguug cagaagaaga aucacaagau gacuugaaag augauuuuuu agaaaagcaa 360
caaccaagug accaucauca auccacgcaa ccuaagacuu caccaucaac ugaacaacaa 420
aagcaacaau cauuugcuua uuguuaagaa cuuagacaag uauauccgaa uggugucacu 480
gccgaucauc cagcauauug accacaauuu gauagagaua aagauuuuuu ugcaugugaa 540
ccugauuuuu auuuuuuuuu 555

```

```

<210> SEQ ID NO 41
<211> LENGTH: 390
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

```

```

<400> SEQUENCE: 41

```

```

augaagaaaa uaaucacag cauuuagggc aucaugcuau uuuuuacagg uuguguuuuu 60
agccaagaga aagccacucu gaaaaaggau aucgauuuuu uacaaaaaga aaauuuuaga 120
uuuuuuuaga aaaaagaaaa gcuucaacaa gaaaaagaaa auuuagcaga uaagcaaaaa 180
gaccuuuuuu aagaagugaa aguuuuuuuu ccuucaaaaag aagauuuuuu ggacgaaaaa 240

```

-continued

| | |
|--|------|
| aaagacgaag acaaaaaaaa agacaaagau aaagaggcau cacaagauaa gcaaucaaaa | 300 |
| gaucaaacua agucaucgga uaaagauaa caaaaaacg cuacaucaac agauaaagau | 360 |
| caaaaagcua augacaaa ccaaucauaa | 390 |
| <210> SEQ ID NO 42 | |
| <211> LENGTH: 2982 | |
| <212> TYPE: RNA | |
| <213> ORGANISM: Staphylococcus aureus | |
| <400> SEQUENCE: 42 | |
| augaagaacg cauuaaaau auuaaaaug gaucugaaga aaguagcuaa gacgccagcu | 60 |
| guguggauua ucuuagcagg cuuagcuuu uugccaucgu ucuacgcuug guuuuacuaa | 120 |
| ugggcaaugu gggauccaua uggcaacacg ggacacauca agguccgagu cguaauggaa | 180 |
| guaaaaggcg acacaucag agggaaaaaa guuaaugucg guaaucgcu gguuaacaca | 240 |
| cucaagaaaa auaaaaguuu ugaauaggcag uuuguaagua gagagaaagc ugaucagag | 300 |
| auaaaaaugg guaaaauuuu ugcagguaau uacauccau cuaaguuuac acaugaaauu | 360 |
| accgggacac uacguaagca gccucaaaaa gcagauguag auuuuaggu gaucagaag | 420 |
| auuaacgcuug uugcgucuaa gcuacagau acugguucgu caguugucgu ugaaaaaggc | 480 |
| aaugaacaau uuaaaaaaac aguaacucga gcauuuuuag aagaagcuaa caaagcaggu | 540 |
| uuacuauuug aagaaaangu gccgacaauu auuaagauaa aaaaugcggg auauucggca | 600 |
| gauaaagcuu uaccuaagau uaaugacuuu gcgaauaaaa uuguauuuu gaauaacac | 660 |
| caagcggauu uagauaaaa ugcgaugau uuuaagaaac uaggaaauu uaaaggugau | 720 |
| auuuuagau cucagaaaa auuaaacgaa gucaauaggug cuauuccgca acuaauggaa | 780 |
| aaggcuuag ugaauuuagc uuuaaaauu uauaugcga aauuagaaa agcguuaauu | 840 |
| uuugcagcuug augacgugcc agcgcaguuc ccuaaaauu aucaaggacu uaacauugcg | 900 |
| agucaaggua ugaucagc uaauggacag uuuaaugaug ccaaggcgu cgucacaca | 960 |
| guuaagaua gagucgguga uuaucaagaa gcaauucgac gcgcgcaaga uuugaucga | 1020 |
| agaaaccagc aacagauucc ucaaaauagc gcggcgaaca acgaaacauc aaauagugca | 1080 |
| ccugcagcuug guaauggugu aacaucaacg ccaccaagug caccaaaugg caauacuaca | 1140 |
| ccaaauaaua auguuacgca aaauaccgca ccaaaugua auuauagcacc uguaucgacu | 1200 |
| acaccacaaa guacaagcgg gaaaaaagau ggucaaaugu uugcagauu aacaacaaca | 1260 |
| caagcagca cagcuaacga gaacacacaa auuuuacag auuuaagau uaaaucuaug | 1320 |
| gaagcggcau uaaccggcuc uuuaauuca uuaucaaaa auuuaagau ccaagcgaaa | 1380 |
| gccgcacaaa aagauaguc ggcuuuacgu auuuuucgu auggcauuu agcaucggac | 1440 |
| aagccaucug auuuuagaga gucuuuagau aauguuaagu ccgguuuaga auacacaacu | 1500 |
| cauuuaaauc aacaauuuu cgaucauuu aaagagauug agaagauga aaauugauu | 1560 |
| uuaucaaaag aaauugaua gguaaagca gcuauuauc gaauuauga aucauuuagg | 1620 |
| uuaguuauc auuuuagua ugcuuuaag auugguuuu caggaucugc ugaagcuacu | 1680 |
| aaauuacug aucaucugc aaacuagau ucauauuuu caucauuuag agauuaguu | 1740 |
| aaaaaagauc uuaacagcuc uuuaugauca auaucacaac guuuuagga ugaauugaac | 1800 |
| aaaggcaca cggcauugc uaauguucag ucuagcuaa aucauuuga ucaagucac | 1860 |
| aacagugguc auucuauuu aaaaaauggu aaaaacgcu ucgauuguu acaaacagua | 1920 |
| uuaccaagua uugaacaaca aucauuuagu gcuuuuaaa augcucaagc aaacuuccg | 1980 |

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| | | | | | | |
|------------|-------------|-------------|--------------|--------------|-------------|------|
| ucuaaucaag | caguugacuu | aggagcuaaa | accaguaaaa | gugcuaacga | aguugcuaaa | 1140 |
| gguauggaag | aaugggcagc | uuuaggcuuu | aaugcctaac | aaacaauugga | ggcuaugcc | 1200 |
| gguguuauca | gugcagcaga | agcaaguggu | gcagaaaugg | cuacaacugc | aacuguaaug | 1260 |
| gcuucagcga | uaaacucuuu | cguuuuaaaa | gcaucugaug | caaucaugu | ugcugauuu | 1320 |
| cuugcgagau | cagcaaauga | uagugcugca | gauauucagu | acaugggaga | ugcauugaag | 1380 |
| uaugcuggua | cuccugcaaa | agcauuagga | guuucuuuag | aggacacuuc | cgcagcauu | 1440 |
| gaaguuuuau | cuaacucagg | uuuagagggg | ucucaagcag | guacugcccu | aagagcuuca | 1500 |
| uuuaucaggc | uagcuaaucc | aaguaaaaau | acagcuaaag | aaaugaaaa | uuuagguuu | 1560 |
| cauuugucug | augcuaaagg | ucauuuuguu | ggcauggggg | aaugauuag | acaguuccaa | 1620 |
| gauaaauaga | aaggcaugac | gagagaacaa | aaacuagcua | caguggcuac | aaugauuggu | 1680 |
| acugaagcag | caaguggauu | uuuagccuug | auugaagcgg | gaccagauaa | aaauuuuagc | 1740 |
| uuuaguuuuu | ccuuuaagaa | uuccaauugg | gaaaguuuuu | aagcagcaga | uuugaugaaa | 1800 |
| gauaaucuca | aaggcgcucu | ggaacaauua | gguggcgcuu | uugaaucauu | agcaauccgaa | 1860 |
| gucgguaaag | auuuuacgcc | uauuuuaga | gcaggagcgg | aagguuuuac | aaaauuuaguu | 1920 |
| gauggauuuu | cacaucuccc | ugguuugguu | agaaaagcuu | caguaggauu | agcacuuuuu | 1980 |
| ggugcaucua | uuggccucgc | uguucuuugc | gguggcuuuu | uaauacuguc | aguuggaagu | 2040 |
| gcugcuaaag | gcuauugcauc | auuuuuuaga | cgcauugcug | aaaauacaa | acugucuaau | 2100 |
| accauuucaa | aagcaauuga | auuuuuuaggu | cuucaaaccu | uuuuuuuugg | uuuuaacaaca | 2160 |
| ggaaaaacgu | caaaagcguu | uaaaggauua | gccggagcua | uguuuuuuuu | uuuuuuuaccu | 2220 |
| auuuuuuuuu | ugaaaaauuc | ugcaaaagcua | gcauuuuuac | cguucaaacu | uuuugaaaaac | 2280 |
| gguuuagga | uagccgcaaa | auccuuuuuu | gcaguuuagug | gaggcgcgaag | uuuugcuggu | 2340 |
| guagccuuua | aguuuuuuac | aggaccuua | ggugcuacaa | uaacugcuau | uacaauugca | 2400 |
| uuuuuuuuuu | uuuuuuuaccg | auuuuuuagc | guguuuuuaggu | ucaguuuuuagc | uuuuuuuaggu | 2460 |
| uuuugagaaa | cuuuuuuaguu | uuuugugugc | uuuuuuuuug | guggugcug | uaggaagcua | 2520 |
| ggaguuuuu | uuuuuuuac | uggaauuuu | ggcauuuagc | ucauuuuuuu | guuuuuuag | 2580 |
| gauuuuagaa | auuuuuuag | auuuuuuag | gacuuuuuagc | uuuuuuuag | aggaguuuac | 2640 |
| aauuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 2700 |
| aauguuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 2760 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 2820 |
| gaaguuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 2880 |
| gaauuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 2940 |
| agugcguuuc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3000 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3060 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3120 |
| agacuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3180 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3240 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3300 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3360 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3420 |
| uuuuuuuuuu | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | uuuuuuuagc | 3480 |

-continued

| | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|------|
| cguguauuaa | aaaauacuga | aaaauuggug | aauaggccuaa | aaaguuggug | gucuaacuuc | 3540 |
| agagaagacc | aaaagaagaa | aagugauaag | uacgcuaaag | aacaagaaga | aacagcucgu | 3600 |
| agaaacagag | aaaauauaaa | gaaaugguuu | ggaaaugcuu | gggacggcgu | aaaaaguaaa | 3660 |
| acuggcgaag | ccuuuaguaa | aaugggcaga | aaugcuaauc | auuuuggcgg | cgaaaugaaa | 3720 |
| aaaauuggga | guggaaucua | aggaauucca | agcaaaauaa | guucagguug | gagcucagcc | 3780 |
| aaaaguucug | uaggauauca | cacuaaggcu | auagcuaaua | guacugguaa | augguuuuga | 3840 |
| aaagcuuggc | aaucuguuua | aucgacuaca | ggaaguauuu | acaaucaaac | uaagcaaaa | 3900 |
| uaucagaug | ccucagauaa | agcuugggcg | cauucaaaau | cuauuuggaa | agggacauca | 3960 |
| aaaugguuua | gcaaugcaua | uaaaugugca | aagggcuggc | uaacggauau | ggcuaauaaa | 4020 |
| ucgcgcucga | aaugggauaa | uauuucuagu | acagcauggu | cgaaugcaaa | auccguuugg | 4080 |
| aaaggaacau | cgaaaugguu | uaguaacuca | uacaaaucuu | uaaaagguug | gacuggagau | 4140 |
| auguaaucaa | gagcccacga | ucguuuugau | gcaauuucaa | guucggcaug | gucuaacgcu | 4200 |
| aaaucaguau | uuaaugguuu | uagaaaaugg | cuaucaagaa | cauaugaau | gauuagagau | 4260 |
| auugguaaag | acaugggaag | agcugcggcu | gauuuaggua | aaaauuguc | uaauaaagcu | 4320 |
| auuggcgguu | ugaauagcau | gauuggcggg | auuaaaaaa | uaucaaaagc | cauuacugau | 4380 |
| aaaaaucuca | ucaagccaau | accuacauug | ucuacuggua | cuuugcagg | aaagggugua | 4440 |
| gcuaccgaua | auucgggagc | auuaacgcaa | ccgacauuug | cuguauuaaa | ugauagaggu | 4500 |
| ucuggaaaacg | cccagggcgg | uggaguucaa | gaaguauuuc | acagggcuga | cggaacaauc | 4560 |
| caugcaccoc | aagagcagaga | ugugguuugu | ccacuaggag | uggagauag | uguaauaaa | 4620 |
| gccaauagaca | cucugaaguu | acagcggau | gguguuuugc | caaaauucca | uggugguacg | 4680 |
| aaaaagaaaa | aauggaugga | acaaguuauc | gaaaauucug | guaaaaaagc | aggggacuuc | 4740 |
| gguucuaaag | cuaaaaacac | agcucuaauu | aucaaaaaag | gugcagaaga | aaugguuuga | 4800 |
| gccgcaggcgg | auaaaaucua | agauggugca | ucuugguuag | gcauuaaaa | cgcgauug | 4860 |
| ugggauuau | uacaacaucc | agggaacua | guaaaaaag | uaaugucagg | uuuaauuu | 4920 |
| aaauuuggag | gcgaggcuua | cgcuacagua | aaaauugcua | aaggcggua | cucauugcuc | 4980 |
| aaaaagaaa | uaguagaca | aguaaaaucg | ugguuugaag | auuuuggug | uggagcgau | 5040 |
| ggaagcuauc | uauuugacca | uccaauuug | caaagguug | ggagcuacac | agguggacu | 5100 |
| aacuuaaag | gcgugcuca | cuauuguauc | gacuuaaaa | ugccuacugg | aacgaacau | 5160 |
| uauugcuua | aaggcgguau | agcugauaaa | guauggacug | auuacggug | cgguauuuc | 5220 |
| auacaaaua | agaccggugc | uaacgaau | aacuggua | ugcauuuau | uaagcaaua | 5280 |
| gcaagacaag | gccaacguau | uaaagcuggu | caacugauag | ggaaaucagg | ugcuacagg | 5340 |
| aaauucguua | gaggagcaca | cuuacauuuc | caauugaugc | aaggugcga | uccagggau | 5400 |
| gauacagcua | aagaucaga | aaaauuggu | aagucacuua | aagguagug | cguucgaagu | 5460 |
| gguucaggug | uuaauaaggc | ugcaucugcu | ugggcaggcg | auauacgucg | ugcagcaaaa | 5520 |
| cgaaugggug | uuaauuuac | uucgggugau | guaggaaaa | uuuuuagcu | gauucaacac | 5580 |
| gaaucaggag | gaaauagcagg | uuaaacuaa | ucuagugcgc | uuagagacau | caacguuuua | 5640 |
| cagggcaauc | cagcaaaagg | auugcuuaa | uauaucccac | aaacauuuag | acaauaugcu | 5700 |
| guuagagguc | acaacaauu | auauaguggu | uacgaucagu | uauuagcgu | cuuuacaac | 5760 |
| agcuauuggc | gcucacaguu | uaaccaaga | ggugguuggu | cuccaagug | uccaagaaga | 5820 |

-continued

| | |
|--|------|
| uaugcgaug gugguuugau uacaaagcau caacuugcug aaguggguga aggagauaaa | 5880 |
| caggagaug uuaucuuuu aacuagacgu aaacgagcaa uucauuuac ugaacagguu | 5940 |
| augcgcauca ucgguaugga uggcaagcca aauaacauga cuguaaaaa ugaucuuca | 6000 |
| acaguugaaa auuuguugaa acaaauguu auguuagug auaaaggaaa uaaauuaca | 6060 |
| gaugcauga uucaaacugu uucuuucag gaaaaaacu uagguucua ugaugcauu | 6120 |
| agagguuuag aaaaauuuu gucaaaacaa agugggcau gagcaaaugc aaaaauuuu | 6180 |
| augggagguu ugacuaauua a | 6201 |

<210> SEQ ID NO 44

<211> LENGTH: 1830

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 44

| | |
|---|------|
| augaaaaagc aauuuuuuu gcuaggcgca uuagcaguug caucuagcu auuuacaug | 60 |
| gaaacaaaag cagaugcgau aguacuaaa gauuuuagua aagaaucaag agugaugag | 120 |
| aacaguaaaa acgauacacc auuuccagau ugguaucua guaguuuuu aacagauua | 180 |
| ggggaucaaa uauacuacgc uaaggaauua acuaaaaau acgaaauagg ugagaagag | 240 |
| uuaagcaag cgauagauaa auugaugacu agaguuuugg gagaagauca uuaucauuu | 300 |
| gaaaaaaga aagcacaaua ugaagcauac aaaaaauggu uugaaaaaca uaaaagugaa | 360 |
| auuccacauu cuaguuuuu aaagauuuuu uuugacgau uugauuuua uagauuacg | 420 |
| aagaagaau acaaugagu acaucaauca uuaaaagaag cuguugauga guuuuuagu | 480 |
| gaagugaaaa auuuucaauc uaaacaaaag gauuuuuuac cuuugauga agcaacugaa | 540 |
| aaucgaguaa caaauggaau auauguuuu guuuugcgaga uugacacau auacgcagca | 600 |
| uuuuuuauuc auagcacaau uggucuuuu gcuaaagaau uaagagcaa gcuagauua | 660 |
| auucuuugug augcuuuaa uccuguuuga auuacgaug aaagaauaag aaaagaaug | 720 |
| auggaugauu uaaauucuu uauugaugau uuuuuuuug auacaaacau gaauagacca | 780 |
| uuaaacauaa cuuuuuuuu uccgaauuu caugacuua cuuuuagcc ugaaauuga | 840 |
| gaaacuuucg auuuuuuuu caaagaaaca agagaagcaa ucgcaaacgc ugacgaauc | 900 |
| uggaaacaa gaaccgucua aauuuacggu gaaucugaaa caaaucucc uguuguaaaa | 960 |
| gaagagaaga aaguugaaga accucauuu ccuaaaguug gaaaccagca agaggauaaa | 1020 |
| auuacaguug guacaacuga agaagacca uuaccaauug cgcaaccacu aguuuuuuu | 1080 |
| ccacagggca cauuucaaag ugaauuuuua aaagguccgg aauaucuaac gauggaaaa | 1140 |
| aaaacguuac aaggugaaau cguucaaggu ccaguuuucc caacaauuga acaaacaga | 1200 |
| ccaucuuuaa gcgauuuuu uacucaaccg acgacaccga acccuuuuu aaaagguuu | 1260 |
| gaaggaacu caacuuaacu ugaauuuuuu ccacaaggua cugaaucaac guuuuuuug | 1320 |
| acucaaggag auucaaguga uauugaagu aaaccucaag caacugaaac aacagaagca | 1380 |
| ucacuuuauc cagcgagacc ucauuuuuac aaaacaccua aguaugugaa auauagagu | 1440 |
| gcugguacag guauccguga auacaacgau ggaacuuuug gauaugaagc gagaccaaga | 1500 |
| uucaacaagc caagcgaaac aaauugcauac aacguaacga caaaucaga uggcacagua | 1560 |
| ucauauugcg cucgccgcg acaaaacaag ccaagcgaau caaacgcau uaacguaaca | 1620 |
| acacaugcaa acggccaagu aucauacgga gcucguccga cacaaaaaa gccaaagcga | 1680 |
| acgaacgcau auaacguaac aacacaugca aacggucaag ugucuaucgg agcucgocca | 1740 |

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```

acacaaaaaca agccaaguua aacaaaugca uacaauguaa caacacaugc agaugguacu 1800
gcgacauaug guccuagagu aacaaaaaaa 1830

```

```

<210> SEQ ID NO 45
<211> LENGTH: 435
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

```

```

<400> SEQUENCE: 45

```

```

augaaaaaag uaaucggacu gcuacuagua aguacauuag cuuuuacagc uuguggugaa 60
aaagaaaaac caaaaaaga agaaaauaaa aagucacaaa cacaaaaaca caaagauagc 120
aaaccaaaaa cgcaacaaga aaaaauugaaa aaaguugaag auaaaaaucc accuaauuuu 180
agcauacaaa auaaaucaaa caaucaaaaac caaucacaaa acaaucaacu uauuuuuuuu 240
ucagaucgau cuaauuuuac uccugcauuu auuuuuuuuu acgauucaca aaauucuuuu 300
uuuuuuuuuu aguauugcgu uucgccuggc uggacuuuuu augaacaggc uaaaguuuuu 360
gaagaguaca aaaaaggaaa agaagacgaa gcaagagcug gugcuagcgc aguaccagga 420
gccaauuuuu acuaa 435

```

```

<210> SEQ ID NO 46
<211> LENGTH: 3774
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

```

```

<400> SEQUENCE: 46

```

```

augggcgaaaa auuuuuuuuu caaacuacca ucaaugguug cauuuacgcu uguagguuca 60
gcagucacug cacaucaagu ucaagcagcu gagacgacac aagaucaaac uacuuuuuuu 120
aauguuuuuu auaguaauaa aguuaaagca acucacugaac aagcaaaagc ugagguuuuu 180
aauccaacgc aaaacuuuuc uggcacucua guuuuuuuuu acccugcuuu uguccaacca 240
aaagcagcga auuuuuuuuu caaugcucaa guuuuuuuuu agguuguuuu uacacaagua 300
aauggugaca cucgucgac ucauuuuuuu acauuuuuuu augcgaaucc uguuuuuuuu 360
ucauuuuuuu caaacgacac uuuuuuuuuu auuuuuuuuu caagucgugg auuuuuuuuu 420
guugauaug aagauguuuu uucaguuuuu cauuuuuuuu cagaauuuuu uuuuuuuuuu 480
gcuuuuuuuu cugcuuuuuu aacgcauuuu aaagccgag cacuuuuuuu aacaccuguu 540
gcaccuuuuu cuuuuuuuuu agcuuuuuuu aaaguuuuuu cuuuuuuuuu uucagcaca 600
ccaagauaug ccgucgagc accuuuuuuu aguuuuuuuu auuuuuuuuu gcauuuuuuu 660
ucauuuuuuu auguuuuuuu ucguuuuuuu auuuuuuuuu caccuuuuuu agaguuuuuu 720
uuuuuuuuuu acuuuuuuuu auuuuuuuuu cguuuuuuuu uuuuuuuuuu uuuuuuuuuu 780
guuuuuuuuu auuuuuuuuu uuuuuuuuuu acuuuuuuuu gcuuuuuuuu uuuuuuuuuu 840
aauuuuuuuu auuuuuuuuu auuuuuuuuu auuuuuuuuu auuuuuuuuu auuuuuuuuu 900
gcuuuuuuuu auuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 960
guuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 1020
gcuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 1080
guuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 1140
gcuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 1200
uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu 1260

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| | | | | | | |
|-------------|-------------|------------|------------|-------------|------------|------|
| acuacccua | cuacaccauc | aaaaccauca | acaccgucga | aaccaucaac | accucaacu | 1320 |
| gguaauuaa | caguugcugc | uaauauggu | gucgcacaaa | ucaaacuac | aaauaguggu | 1380 |
| uuauuacua | cuguuuacga | caaaacuggu | aaagcaacua | augaaguuca | aaaaacauu | 1440 |
| gcuguaucua | aaacagcuac | uuuagguau | caaaaauuc | aucuuguuca | agauuacaau | 1500 |
| ucugguaaua | aaauugguug | gguaaagaa | ggcgaugugg | uuuacaacac | agcuaaauc | 1560 |
| ccuguaaaug | uaaaucuauc | auuucaaac | aaaccuggua | cgaaacuuua | uacaguaccu | 1620 |
| uggguuacau | cuaaacaagu | ugcugguagc | gugucugguu | cuggaaacca | aacauuuag | 1680 |
| gcuucaaagc | aacaacaaau | uguaaaauca | uuuuuuuuu | auggcucugu | gaaugguaaa | 1740 |
| ucugguuggg | uaaguaaagc | auuuuuaguu | gauacugcua | aaccuacgcc | uacaccaaca | 1800 |
| ccuaagccau | caacaccuac | aacaaauau | aaauaacag | uuucaucauu | aaacgguguu | 1860 |
| gcuaaaaua | augcuaaaaa | caauggcuaa | uucacuacag | uuuugacaa | aacugguaag | 1920 |
| ccaacgaaag | aaguucaaaa | aacauuugcu | guaacaaaaa | aagcaagucu | agguggaaac | 1980 |
| aaauucuauc | uaguuuaaga | uuacaauagu | ccaacuuuaa | uugguugggu | uaaacaggu | 2040 |
| gacguuuuuu | auaacaauagc | aaaauccacu | guaaauguaa | ugcaaacuaa | uacaguaaaa | 2100 |
| ccaggcacua | aauuuuuuc | aguaccuugg | gguaacuuua | aacaagaagc | uggugcggu | 2160 |
| ucugguacag | guaaccaaac | uuuuuagcg | acuaagcaac | aacaaauuga | uaaaucuauc | 2220 |
| uuuuuuuag | gaacuguaaa | ugguaaauc | ggugggaaau | guaaagcaua | uuuagcugua | 2280 |
| ccugcugcac | cuaaaaaagc | uguagcacia | caaaaaacug | cuguaaaagc | uuuagcuguu | 2340 |
| acuaaacuc | aaacgacuca | aacaguuagc | aaaauugcuc | aaguuuaacc | aaacaacacu | 2400 |
| gguaauucgug | cuucuguuua | ugaaaaaaca | gcgaaaaacg | gugcaaaaau | ugcggaucgu | 2460 |
| acauucuaug | uaacaaaaga | acgugcacau | gguaaagaaa | cauacguuu | uuuaaaauu | 2520 |
| acaagucuaa | auauuccauu | agguugguuc | aauguaaaag | acuuuuuuga | ucaaacuua | 2580 |
| ggcaagaag | uuuuuagc | ucaaaaaau | acuguaaaca | gaucaaaaau | cgccuuauca | 2640 |
| augguuccuu | ggguuacuaa | aaaccaaguc | uuuuuacag | gcauuuacau | ugcucaaggu | 2700 |
| acuuuuuag | caacgaaaca | aguauucgua | ggcaagaug | uuuuuuuua | cgguacuauu | 2760 |
| auaaccgca | cugguugggu | aaaucaaaa | gauuuuacug | caccaacugc | uguuaaacca | 2820 |
| acuacaucag | cugccaaaga | uuuaaacuac | acuuuuguaa | uuuuuuuag | uaaugguuu | 2880 |
| uacuauguaa | caccaaaauc | ugauacagcu | aaauacucau | uaaaagcauu | uaaugaacaa | 2940 |
| ccauucgcag | uuguuaaaga | acaagucuu | aauggacaaa | cuugguacua | ugguaaaaua | 3000 |
| ucuaacggua | aaauagcaug | gauuuuuuua | acuguuuuag | cuaaagaauu | aauuuaguu | 3060 |
| aaucuuuag | guauagcauu | aaaccaaguu | gcucuuuac | aagcugguuu | acaauuuua | 3120 |
| ccacaaguac | aacguguacc | agguuagugg | acagaugcua | acuuuuuuga | uguuaagcau | 3180 |
| gcauugguaa | cgaagcguuu | agcucaagau | ccagcauuua | aaaucauuu | cuuacgcuaa | 3240 |
| gaccaaccac | aaaauuuuc | uuuuguuuu | uuuuuacuu | ucuuuuuag | uaaaggugua | 3300 |
| uuagaaaacc | aaggugcugc | uuuuuacaaa | gcugcucaaa | uguauuggcau | uaaugaaguu | 3360 |
| uauuuuuuc | cacaucccu | uuuagaaca | gguaacggua | cuucucuuu | agcaaaaggu | 3420 |
| gcagauguag | ugaacaacaa | aguuguuacu | aacucuaaca | cgaaauacca | uaacguuuu | 3480 |
| gguaauucg | cauauuuua | cgauccuuua | cgugaaggua | uuuuuuuag | uaaacaagcu | 3540 |
| gguuugggaca | caguaucaaa | agcaauucgu | gguggugcua | aaucuuuag | caacuauuu | 3600 |
| guuuuagcug | gucaaaauac | gcuuuuacaa | augagaugga | aucugcaca | uccaggaaca | 3660 |

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 caccaauaug cuacagaugu agauugggcu aacaucaaug cuaaaaucou caaaggcuac 3720

uaugauaaaa uuggcgaagu cggcaaauc uucgacauc cacaauuaa auaa 3774

<210> SEQ ID NO 47

<211> LENGTH: 1461

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 47

augucuaaua auuuuaaaga ugacuuugaa aaaaaucguc aaucgauaga cacaaaauca 60

caucaagacc auacggaaga uguugaaaaa gaccaaucag aauuagaaca ucaggauaca 120

auagagaaua cggagcaaca guuuccgcca agaaaugccc aaagaagaaa aagacgccgu 180

gauuuagcaa cgaaucauaa uaaacaaguu cacaaugaau cacaaacauc ugaagacaau 240

guucaaaug aggcuggcac aauagaugau cgucaagucg aaucaucaca caguacugaa 300

agucaagaac cuagccauca agacaguaca ccucaacaug aagagggaua uuuaauaag 360

aaugcuuuug caauggauaa aucacaacca gaaccaaucg aagacaauga uaaacacgag 420

acuauuaaag aagcagaaaa uaacacugag cauucacag uuucugauaa gagugaagcu 480

gaacaauuc agcaaccuaa accauuuuu gcaacaggug cuaaccaagc aaaucauca 540

aaagauaaac augaugaugu aacuguaaag caagacaaag augaaucuaa agaucaucau 600

agugguaaaa aaggcgcagc aauuggugcu ggaacagcgg guguugcagg ugcagcuggu 660

gcauugggug uuucuaaagc uaagaaacau ucaaaugacg cucaaaacaa aaguaauuc 720

ggcaagguga auaacucgac ugaggauaaa gcgucugaag acaagucaaa agaacaucau 780

aaugguaaaa aaggugcagc aaucggugcu ggaacagcag guuuggcugg aggcgcagca 840

aguaauagug cuucugccgc uucaaaacca caugccucua auaaugcaag ucaaaacaa 900

gaugaacaug accaucauga cagagauaaa gaacguaaaa aagguggcau ggccaaagua 960

uuguuaccu uaaauugcagc uguacuaauu aucggugcau uagcgauuu uggaggcaug 1020

gcauuuaaca aucuaauuaa ugguaacaaa gaaaauaaaa ucgcgaauc aaauaaaaa 1080

aaugcugaug aaaguaaaga uaaagacaca ucuaaagacg cuucuaaaga uaaaucaaa 1140

ucucagaca gugauaauc aaaagaugau caagacaaag cgacuaaaga ugaaucugau 1200

aaugaucaaa acaacgcuaa ucaagcgaac aaucagcac aaaaauuca aaaucaaca 1260

caagcuauuc aaaaucaca acagcaacaa caacgucaag gugguggcca aagacauaca 1320

gugaaugguc aagaaaacu auaccguuac gcauucaau acuacgguuc agguucaccg 1380

gaaaauug aaaaaauag acgugccaau gguuaagug gaaacaauu uagaaacggu 1440

caacaaucg uuauccaau a 1461

<210> SEQ ID NO 48

<211> LENGTH: 3825

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 48

augagcuggu uugauaaaau auucggcgaa gauaaugauu caaauauga cuugauucau 60

agaaagaaaa aaagacguca agaaucaca aauauagaua acgaucauga cucauuacug 120

ccucaaaaau augauuuua uagucgucg aggggaaaa uccguuuucc uaugagcgua 180

gcuuaugaaa augaaaau ugaacaauc gcagauacua uuucagauga aaaagaaca 240

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| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|------|
| uaccaucgag | acuaucgcaa | acaaagccac | gauucucguu | cacaaaaacg | acaucgccgu | 300 |
| agaagaaauc | aaacaacuga | agaacaaaau | uauagugaac | aacgugggaa | uucuaaaaau | 360 |
| ucacagcaaa | guauaaaaua | uaaagaucau | ucacauuacc | auacgaauaa | gccagguaca | 420 |
| uauguuucug | cauuuaaugg | uauugagaag | gaaacgcaca | agucaaaaac | acacaauuaa | 480 |
| uauucuaaau | auacaaaauca | ucgugcuaaa | gauucaacua | cagauuauca | caaagaaagu | 540 |
| uucaagacuu | cagagguacc | gucagcuauu | uuuggcacia | ugaaaccuaa | aaaguuaгаа | 600 |
| aauggucgua | ucccuguaag | uaaaucuuca | gaaaaaguug | agucagauaa | acaaaaauau | 660 |
| gauaaaauug | uagcuaagac | gcaaacgucu | caaaaaaac | auuuagaaca | agagaaacaa | 720 |
| aaagauagug | uugucaagca | aggaacugca | ucuaaaucan | cugaugaaaa | uguaucauca | 780 |
| acaacaaaau | caacaccuaa | uuauucaaaa | guugauaaua | cuaucaaaau | ugaaaacauu | 840 |
| uaugcuucac | aaauuguuga | agaaauuuga | cgugaacgag | aacguaaagu | gcuucaaaaг | 900 |
| cgucgauuuu | aaaaagcguu | gcaacaaaag | cgugaagaac | auaaaaacga | agagcaagau | 960 |
| gcaauacaac | gugcaauuga | ugaaauguau | gcuaaacaag | cggaaacgcu | uguuggugau | 1020 |
| aguucauuua | augaugauag | ugacuuacaa | gauaaugua | cagaggcuag | ucagcuucau | 1080 |
| acaaaugaaa | uagaggauга | agcuguauca | aaugaugaaa | auaaaaagc | gucaaucaca | 1140 |
| aaugaagaca | cugaugacac | ucauguagau | gaaaguccau | acaauuauga | ggaaguuaгу | 1200 |
| uugaaucaag | uaucgacaac | aaaacaauug | ucagaugaug | aaguuaacggu | uucggaugua | 1260 |
| acgucucaac | gucaaucagc | acugcaacau | aacguugaag | uaaaauaaca | agaugaacua | 1320 |
| aaaaaucaau | ccagauuuau | ugcugauuca | gaagaagaug | gagcaacgaa | ugaagaagaa | 1380 |
| uauucaggaa | gucaaaucga | ugaugcagaa | uuuuauгаau | uaaaugauac | agaaguagau | 1440 |
| gaggauacua | cuucaaauag | cgaagauaau | accaauagag | acgcgucuga | aaugcaugua | 1500 |
| gacgcuccua | aaacgcaaga | gcacgcagua | acugaaucuc | aaguuaauaa | uaucgauaaa | 1560 |
| acgguugaua | augaaauuga | auuagcgcca | cgucauaaaa | aagaugacca | aacaaacuuu | 1620 |
| agugucaacu | cauugaaaac | gaaugaugug | aaugaugguc | auguugugga | agauucaagc | 1680 |
| augaauгaaa | uagaaaagca | aaacgcagaa | auuacagaaa | augugcaaaa | cgaagcagcu | 1740 |
| gaaгуaaac | aaaauгucga | agagaaaacu | auugaaaacg | uaaauccaaa | gaaacagacu | 1800 |
| gaaaaggguu | caacuuaaag | uaaaagacca | uuuaauguug | ucaugacgcc | aucugauaaa | 1860 |
| aagcguauга | uggaucguaa | aaagcauuca | aaagucaaug | ugccugaauu | aaagccugua | 1920 |
| caaгуaaac | aagcugcgag | ugaagcaag | acugcgacuc | aaaacacacc | aucaucaagu | 1980 |
| acugauucac | aagagucaaa | cacgaaugca | uaaaaaacaa | uaauauugac | aucaaaacau | 2040 |
| guugagaaca | aucaacuuau | uggucaugca | gcaacagaaa | augauuauca | aaaugcacia | 2100 |
| caauauucag | agcagaaaacc | uucugcugau | ucaacucaaa | cggaauauuu | ugaagaaagc | 2160 |
| caagaugaua | aucaauugga | aaaugagcaa | guugaucaau | caacuucguc | uucaguuuca | 2220 |
| gaaguaaгcg | acauaacuga | agaaagcgaa | gaaacaacac | aucaaaacaa | uacuagugga | 2280 |
| caacaagaua | augaugauca | acaaaaagau | uuacagcuuu | cauuuucaaa | ucaaaaugaa | 2340 |
| gauacagcua | augaaaauag | accucggacg | aaucaaccag | auguugcaac | aaaucaagcu | 2400 |
| guacaaacuu | cuaagccgau | gauucгуaaa | ggcccaaaa | uuaaaauгcc | aaguguuuca | 2460 |
| uuacuagaag | aaccacaagu | uauugagccg | gacgaggacu | ggauuacaga | uaaaaagaaa | 2520 |
| gaacuuuaug | acgcauuuuu | uuacuuuaau | guaccugcag | aaguacaaga | uguaacugaa | 2580 |
| gguccaagug | uuacaagauu | ugaauuauca | guugaaaaag | guguuaaagu | uucaagaauu | 2640 |

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acggcauuac aagaugacau uaaaauggca uggcagcga aagauauucg uauagaagcg 2700
ccaaauccag gaacuagucg uguugguuu gaaguuccga accaaaaucc aacgacgguc 2760
aacuuacguu cuauuuuuga aucuccaagu uuuuuuuuug cugaauucua auuacaguu 2820
gcgauggggg auagaauuaa uaaugaacca uuacuuuugg auauugcuaa aacgccacac 2880
gcacuaauug caggugcaac uggaucaggg aaucaguuu guaucaauag uuuuuugaug 2940
ucuuuacua uaaaaauca uccugaggaa uuaagauuu uacuuuuga uccaaaaaug 3000
guugaauuag cuccuuuaa ugguuugcca cauuuaguug caccgguaau uacagauguc 3060
aaagcagcua cacagaguuu aaaugggcc guagaagaaa uggaaagacg uuuaaguuu 3120
uuugcacauu accauguacg uauuuuaaca gcauuuaaca aaaaagcacc auaugaugaa 3180
agaaugccaa aaauugcau aguaauugau gaguuggcug auuuauugau gauggcuccg 3240
caagaaguug agcagucua ugcuaagaau gcucaaaaag cgagagcaug ugguuuucau 3300
auguugguag cuacgcaag accaucuguc aauguaauu cagguuuuau uaaagccaac 3360
auaccaacaa gaauugcau uaugguauca ucaaguguag auucaagaac gauuuuagac 3420
agugguggag cagaacgcuu guuaggauu ggcgauaugu uauaucuugg uagcgguaug 3480
auuuuaccga uuagaguuca agguacauu guuucugaug acgaaauuga ugauguuguu 3540
gauuuuauca aacaacaaag agaaccggac uaccuuuug aagaaaaaga auuguugaaa 3600
aaaacacaaa cacaucaca agaugaauu uuuugaugaug uuugugcau uaugguuuau 3660
gaaggacaua uuucaauc auuuauccaa agacauuucc aaauuggcua uauagagca 3720
gcaagaauu ucgaucauu agagcaacuc gguuauuuu cgagugcua ugguucaaaa 3780
ccaagggau uuuauuuuac ggaagcagau uuaauuuuag aauaa 3825

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<210> SEQ ID NO 49

<211> LENGTH: 630

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 49

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augucgauc aaaaauacga cuacaauaaa aaugaagaug gaaguaaga gaaaauagagu 60
acaacagcga aaguaguug cauugcgacg guuuugcuau uacucggagg auuaguauuu 120
gcauuuuuug cauauuga ucauucgaau aaagcuuuaag aacguauuuu gaacgaacaa 180
aagcaggaac aaaaagaaaa gcgucaaaaa gaaaauugcag aaaaagagag aaagaaaaag 240
caacaagagg aaaaagagca gaauugcua gauucacaag caaaccaaua ucagcaauug 300
ccacagcaga aucaauauca auauugcca ccucagcaac aagcacuac aaagcaacgu 360
ccugcuuuaag aagagauga ugauaaagca ucaaaggau agucgaaaga uaaggauagc 420
aaagcaucuc aagauuuuuc agaugauuu cagaagaaaa cugaugauua uaaacaacca 480
gcucagccua aaccacagcc gcaacaacca acaccaagc cauuuuuuu ucaacaaaac 540
aaucaaucaa aucaacaagc gaaaccacaa gcaccacaac aaaaauugcca aucaacaaca 600
auuuuacaaa auuauugcua ugauuauuag 630

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<210> SEQ ID NO 50

<211> LENGTH: 573

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 50

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| | |
|---|-----|
| augaaaauaa aucauuagc aguguuauca augucagcgg uggugcuuac ugcauguggc | 60 |
| aaugauacuc caaaagauga aacaaaauca acagagucua auacuaauca agacacuaau | 120 |
| acaacaaaag auguuuugc auuaaaagau guuaaaacaa gccagaaga ugcugugaaa | 180 |
| aaagcugaag aaacuuacaa aggccaaaag uugaaaggaa uuucuuuga aaauucuaau | 240 |
| ggugaauagg cuuuaaagu gacacaacaa aaucuggug aagagucaga aguacuuguu | 300 |
| gauguaaaaa auaaaaaagu gauuaacaaa aagacugaaa aagaagauac agugaaugaa | 360 |
| aaugauaacu uuaaaauag cgaugcuua gauuacaaaa aagccauua agaaggacaa | 420 |
| aaggaaauug auggugauau uaaagaagg ucacuugaaa aagaugagg uaaacuuguu | 480 |
| uacaauaucg auuugaaaa agguauuaaa aaacaagaag uuacuguuga ugcuaagaac | 540 |
| gguaaaguau uaaagaguga gcaagaucaa uaa | 573 |

<210> SEQ ID NO 51

<211> LENGTH: 3030

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 51

| | |
|---|------|
| augaaaaga aaaaugggau uuaugcauu auugucacuu uaauuuuuu auuugccaua | 60 |
| guuaguaua uuuuuuuugu ucaacaaaa uauggagauc aaucagaaaa aggaucceaa | 120 |
| aguguaagua auaaaaaua uaaauuacau aucgcaauug uuaacgagga ucaaccaacg | 180 |
| acauuaaacg guaaaaaggu ugagcugggu caagcauuua uuaaaagguu agcaaaugag | 240 |
| aaaaacuuaa auuuugaaac aguaacaaga aacguugcug agucugguuu gaaaauggc | 300 |
| ggauaccaag ucaugauugu uaaccagaa aacuuucaa auuuggcau gcauuagac | 360 |
| gcuaaaacac caucgaaaau aucacuacag uuaaaaacag cuguaggaca aaaagaaga | 420 |
| guagcuaaaa acacagaaaa aguuguaagu aauguacuu acgacuuua caaaaacuug | 480 |
| gucgaaauuu auuuacaag caucauugau auuuacaua augcacaaua aaauuggc | 540 |
| gcuuuuuga cgcgugaaca uggugugaau aguaaaucu cgaauuacu auuuuuucaa | 600 |
| auuaacgacu ucccggaaau auuuacagau acgcuuguua auucgauuuc ugcaacaaa | 660 |
| gauuuucaa auugguucca aacauacaau aaucuuuac ugagugcgaa uucagauaca | 720 |
| uucagaguga acacagauua uaauguuucg acuuuuuuu aaaaaacaaa uucuuuuuu | 780 |
| gacgaacaca auacagcgau ggauaaaau uuacaaguu auaaucgca aaaagauagc | 840 |
| guggaacuug auaacuauu caaugcauu aaacagauug acagccaaa ugaucacaa | 900 |
| ucaaguaugc aagauacagg uaaagaagaa uuaaaacaaa cuguuaaaga aaacuugau | 960 |
| aaauuaagag aaucuuuca aucacaagag ucaccauuu caaaagguu gauugaagac | 1020 |
| uaucguuagc auuuacaga aucacuccaa gaugagcuug caaacacaa agacuuacaa | 1080 |
| gaugcgcuua auagcauuua auugaacaau gcuaauucg cugaaaauu agagaacaa | 1140 |
| cuucaugaug auuuugucca agaaccugau ucagauacaa cauuuuucua uaacaugucu | 1200 |
| aaacaagacu uuauagcugc agguuuuuuu gaggaugaag cuuuuuuuu cgaagcauu | 1260 |
| gucaaaagag caaacgguu uaaaaacgaa uuuuuuuuga aaaaaccguu agcagaacac | 1320 |
| auuuuuuuu caguuuacga uaaccaaguu gcgcaagaca caaguuuuu gauuuuugau | 1380 |
| ggugugaag ugcaacguac ugaacgauu aaaguuuuu auuuuuuua auuuuucguu | 1440 |
| gcaacagauc cucauuuuu uuuugaaggc gacuuuuuu uuuuuuuuu aaaaauagac | 1500 |
| uuuuuagc auuuuuuuu acucgauca ucuuuaagc auuuuuuuu ugaagucuu | 1560 |

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| | | | | | | |
|-------------|-------------|-------------|------------|------------|-------------|------|
| ggcguugcua | aaugaaaa | ggaugcugag | aaaguuucu | uaaaagaua | aacaauugcau | 1620 |
| uuacaauugu | uuuuggaca | agcaaacgu | caagaugaac | caaaugaua | gaaagcaacg | 1680 |
| aguguugugg | auguaacauu | gaaucaaac | cuugaugguc | gcuuaucgaa | agaugcauuu | 1740 |
| agccagcaau | ugagugcauu | aucuagguuu | gaugcgcauu | auaaaaugua | cacagauaca | 1800 |
| aaaggcagag | aagauaaacc | auucgacaac | aaacguuuua | uugauaugau | gguugaccaa | 1860 |
| guuaucaaug | acauggaaag | uuucaagac | gauaaaguag | cuguguuaca | ucaauuugau | 1920 |
| ucaauuggaag | aaaacucaga | caaacugauu | gaugacauuu | uaaaauaaca | aaagaauaca | 1980 |
| acaaaaaua | aagaagauu | uucuaagcug | auugaucagu | uagaaaacgu | uaaaagacu | 2040 |
| uuugcugaag | agccacaaga | accaaaaauu | gauaaaggca | aaaauauga | auuuauacg | 2100 |
| augucuucua | auuagauaa | agaauuagu | agaauuucug | agaaaaguac | gcaauugcua | 2160 |
| ucagauacac | aagaaucaaa | aacaauugca | gauucaguua | guggacaauu | aaaucauuu | 2220 |
| gauaaaaaug | ugaauaaacu | acaugcgaca | ggucgagcau | uaggcguaag | agcgaaugau | 2280 |
| uugaaccguc | aaauggcuaa | aaacgauaaa | gauaaugagu | uauucgcuaa | agaguuuuuu | 2340 |
| aaaguauuac | aaaauucuaa | agauggcgac | agacaaaacc | aagcauuuuu | agcauuuug | 2400 |
| aguauuccgg | uucaaaagaa | aaacuuaagaa | aauguuuuag | cuaauaaugg | uaauacagac | 2460 |
| gugauuucac | cgacaauuguu | cgauuuuug | auguauuuc | uaucaaugau | uacagcauu | 2520 |
| auuuucuaa | gcuauaagc | ugcuuaagga | caaaugaauu | ucaucaaaga | ugauuuuagu | 2580 |
| aguaaaaaca | aucuuuggaa | uaauugcauu | acgucuggug | uuauuggugc | aacugguuuu | 2640 |
| guagaaggau | uaauugcgg | uuuuauugca | augauaaagu | uccauguauu | agcuggcuuu | 2700 |
| agagcgaaa | ucaucuuuu | ggugauuuuu | acuaugaugg | ucuuugcuuu | uauuuuacg | 2760 |
| uauuuacuaa | gacagguuuu | aucuaucggu | auguucuuuu | ugauugcugc | auugggucua | 2820 |
| uacuuguuag | cuaugaauuu | uuugaagcg | gcuggacaag | gugugacuaa | uaaaauuua | 2880 |
| ccauuauuuu | auaucgauuu | cauguuucuu | aaauuuuuuu | augcagagca | uccuauaggc | 2940 |
| uuggcgcuag | uaauuuuac | aguacuugug | uuuuuuggcu | uuguacugaa | cauguuuuuu | 3000 |
| aaacacuuuu | agaaagagag | uuuuuucuaa | | | | 3030 |

<210> SEQ ID NO 52

<211> LENGTH: 1191

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 52

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| augacgcaac | aacaaaaua | uaaaagaaca | uuaaaaaua | aacacacuua | ucaaaaugaa | 60 |
| ccauuaccaa | accguaaaga | uuuuguuguu | aguuuuuuaa | cuggcgcgcu | uguugguua | 120 |
| gcuuuaggcu | uauuuuuua | aaauaaaguu | uaucaaaaag | cagaugauuu | aaaagucaaa | 180 |
| gaacaagaac | ugucgcaaaa | guuugaagaa | agaaaaacgc | aacuugaaga | aacgguuugc | 240 |
| uuuacaaaag | aacguguuga | aggauuuuuu | aacaaaucua | aaaauagaaca | agcggcauug | 300 |
| aaggcacaac | aagcagcauu | aaaagaagaa | gcaagugcaa | auuuuuuuag | cgauacauc | 360 |
| caagaggcac | aagagauuca | agaagcuuuu | agagaagcac | aaacagaaac | ggauuuuuuu | 420 |
| gcgcguguau | caauagaaga | gucuuuagca | ucggcauuua | aggcacaaca | agcagcgaua | 480 |
| aaagaagaag | caagugcaaa | uuuuuuuagu | gaucaucac | aagaagcaca | agcgaaucaa | 540 |
| gaagugaaga | aagaagcgca | agcagaauca | gauuuuuuag | cagaugauuc | aaaugaagaa | 600 |

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| | |
|---|------|
| ucaaaagcau cgacauuaaa cguaucgaaa gaagagucac aagcugaaag auuagcaaac | 660 |
| gcugcaaac agaagcaagc uaaauuaaca ccaggcucaa aagagaguca auuacugaa | 720 |
| gcguuuuug cagaaaaacc aguugcuaaa aaugacuuga aagaaauucc ucuaauaguu | 780 |
| acuaaaaaga augauguauc agaaacaguu aaucagaua auaaagacac uguuaaaca | 840 |
| aaagaagcua auuugaaaa ugguguuuu acacguaaag cugaugaaaa aacaccuaau | 900 |
| aaucagcug uugacaagaa aucagguaaa caaucuaaaa aaacaacacc uucaauuaa | 960 |
| cgaaaugcau caaaagcauc gacaaauaaa acuucagguc agaaaaagca acuaauaag | 1020 |
| aaagcaucac aaggugcaaa gaaacaagu aguucaagua acucaacgac aaagcuaau | 1080 |
| caaaaaauu caaaagcaac aaaugcuaaa ucauccaauug caucaaaaa aucaauugcu | 1140 |
| aaaguugaaa aagcuaaaag uaaaaagag aaacguacau uuaaugacua a | 1191 |

<210> SEQ ID NO 53

<211> LENGTH: 2310

<212> TYPE: RNA

<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 53

| | |
|--|------|
| guggauuuug guaaaaaaca uguauuuccu aaaagucagu accgacguaa gcgucgugaa | 60 |
| uuuuuccaca acgaagacag agaagaaaau uuaaaucac aucaagauaa acaaaaauua | 120 |
| gauaaucaca caucaaaaa agcagauaag caaaucacua aagauucaau ugauaagcac | 180 |
| gaacguuuua aaaaauuuuu aucaucgcau uuagaacaga gaaaccguga ugugaauagag | 240 |
| aacaaagcug aagaaaguaa aaguauucag gguaguaagu cagcauuua caaagaucau | 300 |
| uuuuuacag acgauuauc uaaaaaaca auucauuug auucaguaga ccaagauaca | 360 |
| gagaaucaca auuuuuuga gcaaaauacu gaagcgacu uaucaacua uucaaccgau | 420 |
| aaaguagaau caacugacau gagaaagcua aguucagaua aaaacaaagu uggucaugaa | 480 |
| gagcaacaug uacuuucua accuucagaa cauguaaag agacuagaau ugauuuugag | 540 |
| ucuucaagaa cugauucaga cagcucgaug cagacagaga aaauaaaaa agacaguuca | 600 |
| gauggaaaua aaaguaguaa ucgaaaucu gaaguaauu cagacaauc aaauucagua | 660 |
| ccauuuuug cggaaucuga ugaugaagua auuaucaga agccauuac uuugccgga | 720 |
| gaacagaaau ugaaaaggca gcaaaugcua aaugagcaaa caaaaacua uacauauggu | 780 |
| gauagcgaac aaaaugaca gucuauucau gaaaauuuu uaagucaua uacaccaucg | 840 |
| auaagugaug auaaagaua cguuauuga gaagaucau uuguugcga uauccugau | 900 |
| aaugauauca auacaccauc auuaucaaaa auagaugacg aucgaaaacu ugaugaaaa | 960 |
| auucaugucg aagauaaca uaaacaaaau gcagacucau cugaaacggu gggauuca | 1020 |
| agucagucac gugcaucua ucguagcacu gaaaaagaa auauggcua uaaugaccau | 1080 |
| gauaaaaua acggucaaaa accaaaauca aagacaucgg caaaauuaa ucaaaaaag | 1140 |
| gcuacauca aauugaaca agggcgcgcu acaauuaa auuuuagcgc cauuuugaaa | 1200 |
| aaguuuuga ugauguauug gccuaaaaua guuuuucua uggguuuuu uauucuaau | 1260 |
| guuuuuuga augccauuuu uauuuuug acaaaaaug aucgcaugaa ugauuuuuu | 1320 |
| gaugcagaug cucaaaaaa uacgacaacg augaaaaug ccaauaacgc aguuuuuucg | 1380 |
| gucguuacag uugaaaauga aacaucaaaa gauucauca uaccuaaaga uaaagcaucu | 1440 |
| caagacgaag uaggaucagg uguuguauu aaaaaaucg gagauucguu auuuuuuuu | 1500 |
| acgaugcac acguuugcgg ugauaaagaa aucaaaaaa uaacuuucuc gaauuuuaa | 1560 |

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aguguuguug ggaaagugcu ugguaaagau aaauaggucag auuuagcugu uguuaaagca 1620
acuucucucag acaguucagu gaaagagaua gcuauuggag auucaaauaa uuuaguguaa 1680
ggagagccaa uauuagucgu agguaaacca cuugguguag acuuuaaagg cacugugaca 1740
gaagguauua uuucaggucu gaacagaaau guuccaaauug auuucgauaa agauaauaaa 1800
uaugauaugu ugaugaaagc uuuccaaaau gaugcaucag uaaauccagg uaacucgggu 1860
ggugcugucg ucaauagaga aggaaaaaua auugguguag uugcagcuaa aaauaguau 1920
ccaaacguug aaaaauuguc auuugcaaua ccuguaaauug aaguacaaaa gauuguaaaa 1980
gaauuagaaa caaaagguaa aaugacuau cccgauguag guguaaaaa gaagaauuu 2040
gccagucuaa auaguuuuga aagacaagca guuaaaauugc uaggaaaagu uaagaacggg 2100
guuguuguag aucaaguuga caacaauugu uuagcagauc aaucuggucu gaaaaaaggu 2160
gauguaauua cugaauuaga uggcaaacuu uuagaagaug auuuacgcuu uaggcagauu 2220
auuuuuguc auaagauga cuugaaaaua auuacagcga agauuuuauag agaugguaaa 2280
gaaaaagaaa uuaauuuuaa acuaaaaaaa 2310

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<210> SEQ ID NO 54
<211> LENGTH: 627
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

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<400> SEQUENCE: 54
augaaaauca aagcuaucgu ugcaaucaca uuaucauugu cacuaauaac cgccuguggu 60
gcuaaucaac auaaagaaaa uaguaguuaa ucaaaugaca cuaauaaaaa gacgcaacaa 120
acugauaaca cuacacaguc aaauacagaa aagcaaauga cuccacaaga agccgaagau 180
aucguucgaa acgauuacaa agcaagaggu gcuaacgaaa aucaaacuu aaauuuuaaa 240
acaaaucuuug aacgaaguua ugaacaugaa uuuuauuguug aacaucuaugu ccgcaugca 300
guuggcacac cauuuuuacg uugcgcuuu guuaaucgac acaaugguac gauuuuuuu 360
auuuuugaug auaugucaga aaaagauaaa gaagaauuug aagcauuuaa aaagagaagc 420
ccuaaaauaca acccagguau gaauaugaaca gcugaaaugg auuauaguc ggaagacuu 480
caacaucaug auuuugacaa uaacaagcc auucaaaaug acuuaccaga ucaaaaaguc 540
gauguaaaaa acguaaaaa ugcuguuaau aaagaagaaa aacacgauaa ccgugaaaa 600
aaucagcag aaacuaaagu uaaaaaa 627

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<210> SEQ ID NO 55
<211> LENGTH: 684
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

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<400> SEQUENCE: 55
auggaaaga aaaaagucuu caaaauuuug auuaauuuuu uaccauuugu auugguaccg 60
uuuuuuuuug aacguaaaacg uaucaaaaca cauccggagc uacaaaaagu uacagaugcu 120
acaaguuaag uugcuuacaa aacaucugca gcaaucagua acacagcgag ugauguuaaa 180
gaauaugucg gcauuuuuuu acaaguuuuu gaaaauaagc gugaacuuua aaaguuuugu 240
agagaacaug auccugccua uauugagaaa aaagcgcaaa auuuagcuaa acaaaucgu 300
aaagacgcug auuuuuuuga uuuuuuuuuu caaaaaaua ucgaaaagcg ucauuuagaa 360
gagcaaaaag cccgcgaaaa gaauuuuuuu caacguuuuu aaguuuuuuu aaagucacaa 420

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| | |
|---|-----|
| aaauacgaag uaaaagcagg cuuaacaccu aauaaaauag augagaaaac ugagaaaaaa | 480 |
| ggcgauaaac uagcugaaaa aaaucgcaa gaaucgcua aaugaauaa aaaguuacaa | 540 |
| aaaaauuug aaaaacgaca caaagaagaa caaaaacgcc aacaagaagc ugauaaagca | 600 |
| cgcaucaagu cauuuaaaa auauaaagau uauguugcca aaagcgccuc ucaacaaaau | 660 |
| aaagaaaaa auacagaggg auaa | 684 |

<210> SEQ ID NO 56
 <211> LENGTH: 1215
 <212> TYPE: RNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 56

| | |
|--|------|
| augucauauc auugguuuaa gaaauguaa cuuucacaa guauguuaa uuuuaguagu | 60 |
| aguaguagu uagggcuugc aacgcacaca guugaagcaa aggauaacuu aaugggagaa | 120 |
| aagccaacga cuauuuugaa ucauaaugua acucaccau caguauuag ugaaugaau | 180 |
| aaaaaugaga cugggacacc ucacgaauc aaucacagc guauugaagc aacugguucg | 240 |
| aaugucgug augcuauuc ugaucgaa auugugaagc cagacucua caaccaaacc | 300 |
| ccaaguccag auucaaacc ugacccaa aucccaaacc cagguccgaa uccgaagcca | 360 |
| gaccagaua agccgaaacc aaucgga ccaaagccag acccagaua gccgaaacca | 420 |
| auccggauc caaaaccaga uccagacaaa ccgaagccaa auccggauc aaaaccagau | 480 |
| ccaaauccga auccgaauc aaaaccagac ccuaauaagc caaaucuaa uccgucucca | 540 |
| aaucceauc aaccugggga uuccaauca ucuggugcu cgaaaaugg ggggacaugg | 600 |
| aaccaaaug cuucagaugc aucuaauca ggucaaugc aaccaaaugc aaaucaagga | 660 |
| aacucacaaa auccuacugg uauuguuuu guauccaac gauuuuagc cuuggcgaau | 720 |
| ggggcuuaca aguauauuc guauuuuuu aaucuuuuu aucauuuggg gaaagaauu | 780 |
| ggugagguaa cugaugaaga uaucuaca aucauccgaa aacaaaauu cagcggaau | 840 |
| gcuuuuuuu auggauuaca acagcaaucg auuuuuuuu gauuccaaua uuucaauca | 900 |
| uugaaucag aaagguacua ucguuuuuu gaugaacaag uacucgcau auuucuggc | 960 |
| gaaauuggau caaugccaga uuugaaaaag cccgaagaa agccggauc aaaacaacgu | 1020 |
| ucauuugagc cucaugaaaa agauguuuu acaguugua aaaaaaca agauauaag | 1080 |
| aaaagugcgu caacugcau uaguuaaagu uggcuagcaa uuguauuuc uauguggug | 1140 |
| guuuuuuca ucaugcuau cuuuuuugua aagcgaaaua aaaagaaaa uaaaaacgaa | 1200 |
| ucacagcgac gauaa | 1215 |

<210> SEQ ID NO 57
 <211> LENGTH: 696
 <212> TYPE: RNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 57

| | |
|--|-----|
| augaagaaaa cauucucgc aucaucaua gcaguaguu uaggaucgu agcaggaaau | 60 |
| gcaggucacg aagccaagc aagugaagcg gacuuuuuu aagcaucuu agcgcaauug | 120 |
| gcgcaucaa augaucaaac auuuuuuuu aaaccaauug aagcuggcgc uuuuuuuuu | 180 |
| acuuuugacu augaaggguu uacuuuacac uuugaucag augguacaca cuuugcuugg | 240 |
| aauuaccaug caacaggugc uauuggagca gacaugagug cacaagcacc ugcaacuaa | 300 |
| aauguugcac caucagcuga ucauucuaa caaguacaau cacaagaagu ugaagcacca | 360 |

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| | |
|--|-----|
| caaaaugcuc aaacucaaca accacaagca ucaacaucaa acaauucaca aguuacugca | 420 |
| acaccaacug aaucaaaagc aucagaaggu ucaucaguua augugaauga ucaucuaaaa | 480 |
| caaaauugcuc aacgugaauc agguggcaau auucaugcug uaaauccaac aucaggugca | 540 |
| gcugguaagu aucaauucuu acaaucaacu ugggaucag uagcaccugc uaaaauuaaa | 600 |
| gguguaucac cagcaaaugc uccugaaagu guucaagaug cgcgagcagu aaaacuauau | 660 |
| aacacuggug gcgcuggaca uuggguuacu gcauaa | 696 |

The invention claimed is:

1. A pharmaceutical composition consisting of at least one polypeptide and a pharmaceutically acceptable carrier, vehicle or diluent, and an immunological adjuvant, wherein the at least one polypeptide consists of 35-144 contiguous amino acid residues from amino acid residues 343-486 of SEQ ID NO: 9.

2. The pharmaceutical composition according to claim 1, wherein the at least one polypeptides consists of amino acid residues 343-452 of SEQ ID NO: 9.

3. A pharmaceutical composition consisting of at least one polypeptide, and

a pharmaceutically acceptable carrier, vehicle or diluent, and an immunological adjuvant, wherein the at least one polypeptide consists of an amino acid sequence that has at least 80% sequence identity with 35-144 contiguous amino acids from amino acid residues 343-486 of SEQ ID NO: 9.

15 4. The pharmaceutical composition according to claim 1, wherein said at least one polypeptide is a single polypeptide.

5. The pharmaceutical composition according to claim 3, wherein said at least one polypeptide is a single polypeptide.

20 6. The pharmaceutical composition according to claim 3, wherein said at least one polypeptide consists of an amino acid sequence that has at least 80% sequence identity with 35-144 contiguous amino acids from amino acid residues 343-452 of SEQ ID NO: 9.

25 7. The pharmaceutical composition according to claim 1, wherein the immunological adjuvant is an aluminium based adjuvant.

8. The pharmaceutical composition according to claim 2, wherein the immunological adjuvant is an aluminium based adjuvant.

30 9. The pharmaceutical composition according to claim 3, wherein the immunological adjuvant is an aluminium based adjuvant.

* * * * *